

XX The present invention describes a pure protein (P1) comprising a BAX
CC polypeptide lacking an apoptotic regulation of targeting (ART) domain.
CC P1 has cytosolic activity and can be used in the modulation of
CC apoptosis. The polypeptides and methods from the present invention are
CC useful for identifying compounds that modulate apoptosis which can then
CC be used for treating cancer. The present sequence represents a mouse
CC BAX peptide sequence of amino acids 1 to 20, which is used in an
CC example from the present invention.

XX Sequence 20 AA:

Query Match 88.5%; Score 69; DB 21; Length 20;
Best Local Similarity 73.7%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 MDGSGXXXXXGPTSSSEQI 19
Db 1 MDGSGEQLGSGGPTSSSEQI 19

RESULT 2

AAV70817
ID AAV70817 standard; Protein: 70 AA.

XX AAV70817:

DT 31-JUL-2000 (first entry)

DE Mouse neuroprotective truncated BAX protein, tBAX70.

XX Mouse; truncated BAX protein; tBAX70; BAX alpha; BCL-2 family;
KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
KW spinal cord injury; head trauma; stroke.

XX Mus musculus.

OS Mus musculus.

XX Key

FT Region 1..58 Location/Qualifiers
FT Domain 59..70 /note= "N-terminal region of BAX alpha"

FT Domain /label= Partial_BH3 domain
FT /note= "BH3 domain in the full-length BAX alpha consists
of amino acids 59-73"

XX WO200023083-A1.

PD 27-APR-2000.

PF 22-OCT-1999; 99WO-US24747.

PR 22-OCT-1998; 98US-0177315.

PA (UNIW) UNIV WASHINGTON.

PI Johnson EM, Easton R;

DR WPI: 2000-339513/29.

PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
for the treatment of nervous system disorders -

PS Claim 4; Page 32; 43pp; English.

XX The present sequence is a specifically claimed truncated BAX protein
CC tBAX70 which inhibits neuronal apoptosis induced by trophic factor
CC deprivation. The protein consists of first 70 amino acids of mouse
CC BAX alpha, that includes the N-terminal region and a portion of the BH3
CC domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of
CC the full-length BAX alpha. The tBAX protein lacking only the
CC transmembrane domain has been shown to have anti-apoptotic activity.
CC The present sequence is used to treat diseases associated with neuronal

CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
CC spinal cord injury, head trauma and stroke.

XX Sequence 70 AA:

Query Match 88.5%; Score 69; DB 21; Length 70;
Best Local Similarity 73.7%; Pred. No. 4e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 1 MDGSGXXXXXGPTSSSEQI 19
Db 1 MDGSGEQLGSGGPTSSSEQI 19

RESULT 3

AAV70821
ID AAV70821 standard; Protein: 70 AA.

XX AAV70821:

DT 31-JUL-2000 (first entry)

DE Mouse neuroprotective truncated BAX protein tBAX70 mutant.

XX Mouse; truncated BAX protein; tBAX70M; BAX alpha; BCL-2 family; mutant;
KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
KW spinal cord injury; head trauma; stroke.

XX Mus musculus.

OS Synthetic.

XX Key

FT Region 1..58 Location/Qualifiers
FT Domain 59..70 /note= "N-terminal region from BAX alpha"

FT Domain /label= Partial_BH3 domain
FT /note= "BH3 domain in the full-length BAX alpha consists
of amino acids 59-73"

FT Misc-difference 55 /note= "Wild type Ser is substituted by Ala"

FT Misc-difference 60 /note= "Wild type Ser is substituted by Ala"

XX WO200023083-A1.

PD 27-APR-2000.

PF 22-OCT-1999; 99WO-US24747.

PR 22-OCT-1998; 98US-0177315.

PA (UNIW) UNIV WASHINGTON.

PI Johnson EM, Easton R;

DR WPI: 2000-339513/29.

DR N-PADB: AAD00124.

PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
for the treatment of nervous system disorders -

PS Claim 4; Page 34; 43pp; English.

XX The present sequence is a specifically claimed truncated BAX protein,
CC tBAX70 mutant (tBAX70M) which inhibits neuronal apoptosis induced by
CC trophic factor deprivation. The protein consists of the N-terminal
CC region and a portion of BH3 domain from mouse BAX alpha.
CC It lacks the BH1, BH2 and C-terminal transmembrane
CC domains of the full-length BAX alpha. The tBAX protein lacking only the
CC transmembrane domain has been shown to have anti-apoptotic activity.
CC The present sequence is used to treat diseases associated with neuronal
CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,

CC spinal cord injury, head trauma and stroke.
XX
SQ Sequence 70 AA:

Query Match 88.5%; Score 69; DB 21; Length 70;
Best Local Similarity 73.7%; Pred. No. 4e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDGSGXXXXGPTSSSQI 19
||||| |||||||
Db 1 MDGSGEQLGSGCPTSSSQI 19

RESULT 4
AA770819
ID AA770819 standard; Protein; 78 AA.

AC AA770819;
XX
DT 31-JUL-2000 (first entry)

XX Mouse neuroprotective truncated BAX protein, tBAX78.

KW Mouse; truncated BAX protein; tBAX78; BAX alpha; BCL-2 family;
KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
KW spinal cord injury; head trauma; stroke.
XX
OS Mus musculus.

Key Location/Qualifiers
FH Region 1..58
FT /note= "N-terminal region of BAX alpha"
FT 59..73
FT Domain /label= BH3_domain

XX MO200023083-A1.

XX 27-APR-2000.

XX 22-OCT-1999; 99WO-US24747.

XX 22-OCT-1998; 98US-0177315.

XX (UNITW) UNIV WASHINGTON.

XX Johnson EM, Easton R;

XX WPI: 2000-339513/29.

XX N-PSDB: AAD00123.

PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
PT for the treatment of nervous system disorders -
XX
XX
PS Claim 4; Page 33; 43pp: English.

CC The present sequence is a specifically claimed truncated BAX protein
CC tBAX78 which inhibits neuronal apoptosis induced by trophic factor
CC deprivation. The protein consists of first 78 amino acids of mouse
CC BAX alpha, that includes the N-terminal region and BH3
CC domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of
CC the full-length BAX alpha. The tBAX protein lacking only the
CC transmembrane domain has been shown to have anti-apoptotic activity.
CC The present sequence is used to treat diseases associated with neuronal
CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
CC spinal cord injury, head trauma and stroke.
XX

SQ Sequence 78 AA:

Query Match 88.5%; Score 69; DB 21; Length 78;
Best Local Similarity 73.7%; Pred. No. 4.5e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDGSGXXXXGPTSSSQI 19
||||| |||||||
Db 1 MDGSGEQLGSGCPTSSSQI 19

RESULT 5
AA770823
ID AA770823 standard; Protein; 78 AA.

AC AA770823;
XX

DT 31-JUL-2000 (first entry)

XX Mouse neuroprotective truncated BAX protein tBAX78 mutant.

KW Mouse; truncated BAX protein; tBAX78M; BAX alpha; BCL-2 family; mutant;
KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
KW spinal cord injury; head trauma; stroke.
XX

XX Mus musculus.
OS Synthetic.

Key Location/Qualifiers
FH Misc-difference 55
FT /note= "Wild type Ser is substituted by Ala"
FT 60
FT Misc-difference 60
FT /note= "Wild type Ser is substituted by Ala"
FT 71..78
FT Region /note= "sequence not found in BAX alpha"

XX MO200023083-A1.

XX 27-APR-2000.

XX 22-OCT-1999; 99WO-US24747.

XX 22-OCT-1998; 98US-0177315.

XX (UNITW) UNIV WASHINGTON.

XX Johnson EM, Easton R;

XX WPI: 2000-339513/29.

XX N-PSDB: AAD00126.

PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
PT for the treatment of nervous system disorders -
XX
XX
PS Claim 4; Page 34-35; 43pp: English.

CC The present sequence is a specifically claimed truncated BAX protein,
CC tBAX78 mutant (tBAX78M) which inhibits neuronal apoptosis induced by
CC trophic factor deprivation. The protein consists of the N-terminal
CC region and a portion of BH3 domain of mouse BAX alpha, and a novel
CC C-terminal sequence of 8 amino acids not present in BAX alpha.
CC It lacks the BH1, BH2 and C-terminal transmembrane
CC domains of the full-length BAX alpha. The tBAX protein lacking only the
CC transmembrane domain has been shown to have anti-apoptotic activity.
CC The present sequence is used to treat diseases associated with neuronal
CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
CC spinal cord injury, head trauma and stroke.
XX

SQ Sequence 78 AA:

Query Match 88.5%; Score 69; DB 21; Length 78;
Best Local Similarity 73.7%; Pred. No. 4.5e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 MDGSGXXXXGPTSSSQI 19
||||| |||||||
Db 1 MDGSGEQLGSGCPTSSSQI 19

RESULT 6

AAR71407
ID AAR71407 standard; Protein: 192 AA.

XX AAR71407;

XX 15-NOV-1995 (first entry)

XX Murine Bax protein.

DE Human: bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line;
XX apoptosis; membrane-associated cytoplasmic protein; B cell; T cell;
KW proliferation; cell cycle progression; Bax; apoptotic cell death;
KW apoptosis; cytokine; death repressor; BHL; BH2; cancer therapy;
KM hyperplasia; immunodeficiency disease; AIDS; neurodegeneration;
KM ischaemic cell death.

XX Mus musculus.

OS WO9505750-A.

XX 02-MAR-1995.

XX 24-AUG-1994; 94WO-US09701.

XX 26-AUG-1993; 93US-0112208.

PR 25-MAY-1994; 94US-0248819.

XX (UNIW) UNIV WASHINGTON.

PA Korschmeier SJ;

XX WPI; 1995-106605/14.

PT Methods for producing and identifying mutant bcl-2 proteins -
XX that lack death repressor activity and/or lacks binding to Bax.

PS Disclosure; Fig 3; 133pp; English.

XX This sequence represents murine Bax protein. Bax is a protein which is
CC associated with the bcl-2 alpha and beta proteins. bcl-2 is encoded by a
CC proto-oncogene and is capable of inhibiting apoptosis in many
CC hematopoietic cell systems. bcl-2 is a 26 kD membrane-associated
CC cytoplasmic protein and is thought to function by enhancing the survival
CC of hematopoietic cells of B and T origins rather than directly promoting
CC proliferation of these cell types. bcl-2 has not been shown to directly
CC promote cell cycle progression nor does it necessarily alter the dose
CC response to limiting concentrations of IL-3. bcl-2 has been shown to form
CC heterodimers with this 21 kD protein, Bax. Overexpressed Bax accelerates
CC apoptotic cell death induced by cytokine deprivation in an IL-3 dependent
CC cell line, and it also acts to counter the death repressor activity of
CC bcl-2. Therefore, the ratio between bcl-2 and Bax determines cell
CC survival or death following an apoptotic stimulus. The invention gives
CC a mutant form of bcl-2 in which there is at least one amino acid
CC substitution or deletion in the BH1 or BH2 domains. This makes the
CC mutant protein substantially incapable of binding Bax and/or incapable
CC of death repressor activity. Down regulation of bcl-2 is useful in
CC cancer therapy, controlling hyperplasias and eliminating self-reactive
CC clones in autoimmunity by favouring death effector molecules. Up
CC regulating bcl-2 is beneficial in treatment and diagnosis of immuno-
CC deficiency diseases, including AIDS and neurodegenerative and ischaemic
CC cell death.

XX Sequence 192 AA;

Query Match 88.5%; Score 69; DB 16; Length 192;

Best Local Similarity 73.7%; Pred. No. 0.00012;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDGSGXXXXXGPTSSSEOI 19
DB 1 MDGSGEQLGSGGPTSSSEOI 19

RESULT 7

AA05434
ID AA05434 standard; peptide: 192 AA.

XX AA05434;

XX 02-JUL-1999 (first entry)

XX Mouse BAX protein sequence.

DE BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;
XX apoptosis promoter; cancer cell; virus infected cell; inflammation;
KW autoantibody producing cell; cancer; lymphoproliferative condition;
KM arthritis; autoimmune disease; therapy.

XX Mus sp.

OS WO916787-A1.

XX 08-APR-1999.

XX 22-SEP-1998; 98WO-US19765.

XX 07-OCT-1997; 97US-0946039.

PR 26-SEP-1997; 97US-0060133.

XX (UNIW) UNIV WASHINGTON.

PA Korschmeier SJ;

XX WPI; 1999-255058/21.

XX Bcl homology domain 3 polypeptide

PT Disclosure; Fig 21c; 104pp; English.

XX This sequence represents the murine BAX protein.
CC The invention relates to a bcl homology domain 3 (BH3 domain),
CC derived from a proapoptotic member of the BCL-2 family. The
CC BH3 polypeptide can be used in a method for promoting apoptosis in a
CC target cell, especially where the cell is a cancer cell a virus infected
CC cell or an autoantibody producing cell. The BH3 polypeptide can be used
CC in therapeutic compositions for treating disease including cancer, other
CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
CC diseases, which may result from the down regulation of cell death
CC regulation.

XX Sequence 192 AA;

Query Match 88.5%; Score 69; DB 20; Length 192;

Best Local Similarity 73.7%; Pred. No. 0.00012;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDGSGXXXXXGPTSSSEOI 19

DB 1 MDGSGEQLGSGGPTSSSEOI 19

RESULT 8

AAW87805
ID AAW87805 standard; Protein: 192 AA.

XX AAW87805;

XX 10-MAR-1999 (first entry)

XX Murine Bcl-2 associated protein designated Bax.

XX Murine: Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;
KW bcl-2-related function; apoptosis.


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OS Mus sp.
XX
XX US5856171-A.
XX
XX 05-JAN-1999.
XX
XX 10-NOV-1994; 94US-0337646.
XX
XX 10-NOV-1994; 94US-0337646.
XX 26-AUG-1993; 93US-0112208.
XX 25-MAY-1994; 94US-0248819.
XX
XX (UNITW ) UNIV WASHINGTON.
XX
XX Kormeyer SJ;
XX
XX WPI: 1999-105119/09.
XX
XX DNA composition encoding bcl-2 two-hybrid and reporter system - for
XX identifying modulators of bcl-2 function
XX
XX Example 4; Columns 73-74; 105pp; English.
XX
XX The present sequence represents a murine Bcl-2 associated protein
XX designated Bax. The Bax protein is used in a composition which
XX comprises a bcl-2 family member polypeptide, a naturally occurring
XX Bax polypeptide and an antibody that binds to the Bax polypeptide.
XX The composition is used to identify modulators of bcl-2-related
XX function, e.g. substances that inhibit binding of Bax to bcl-2,
XX which would be potentially useful as drugs for modulating
XX apoptosis.
XX
XX Sequence 192 AA:
SQ
XX
XX Query Match 88.5%; Score 69; DB 20; Length 192;
XX Best local Similarity 73.7%; Pred. No. 0.00012;
XX Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 MDGSGXXXXXGPTSSSEQI 19
Db 1 MDGSGEQIGSGGPTSSSEQI 19
XX
XX RESULT 9
XX AAW87808
XX ID AAW87808 standard; Protein; 192 AA.
XX
XX AAW87808;
XX
XX 10-MAR-1999 (first entry)
XX
XX Murine Bcl-2 associated protein designated Bax.
XX
XX Murine; Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;
XX bcl-2-related function; apoptosis.
XX
XX Mus sp.
XX
XX US5856171-A.
XX
XX 05-JAN-1999.
XX
XX 10-NOV-1994; 94US-0337646.
XX
XX 10-NOV-1994; 94US-0337646.
XX 26-AUG-1993; 93US-0112208.
XX 25-MAY-1994; 94US-0248819.
XX
XX (UNITW ) UNIV WASHINGTON.
XX
XX Kormeyer SJ;
XX
XX WPI: 1999-105119/09.
XX

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XX
XX DNA composition encoding bcl-2 two-hybrid and reporter system - for
XX identifying modulators of bcl-2 function
XX
XX Example 10; Fig 7; 105pp; English.
XX
XX The present sequence represents a murine Bcl-2 associated protein
XX designated Bax. The Bax protein is used in a composition which
XX comprises a bcl-2 family member polypeptide, a naturally occurring
XX Bax polypeptide and an antibody that binds to the Bax polypeptide.
XX The composition is used to identify modulators of bcl-2-related
XX function, e.g. substances that inhibit binding of Bax to bcl-2,
XX which would be potentially useful as drugs for modulating
XX apoptosis.
XX
XX Sequence 192 AA:
SQ
XX
XX Query Match 88.5%; Score 69; DB 20; Length 192;
XX Best local Similarity 73.7%; Pred. No. 0.00012;
XX Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY 1 MDGSGXXXXXGPTSSSEQI 19
Db 1 MDGSGEQIGSGGPTSSSEQI 19
XX
XX RESULT 10
XX AAY70828
XX ID AAY70828 standard; Protein; 192 AA.
XX
XX AAY70828;
XX
XX 31-JUL-2000 (first entry)
XX
XX Mouse BAX alpha protein.
XX
XX Mouse; truncated BAX protein; tBAX; BAX alpha; BCL-2 family; head trauma;
XX neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
XX apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
XX spinal cord injury; stroke; pro-apoptotic; PCD; programmed cell death.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Region 1..58
XX Domain 59..73
XX FT /label= BH3_domain
XX FT /note= "BCL-2 Homology domain 3"
XX FT 98..118
XX FT /label= BH1_domain
XX FT 150..165
XX FT /label= BH2_domain
XX FT 169..188
XX FT /label= Transmembrane_domain
XX
XX WO200023083-A1.
XX
XX 27-APR-2000.
XX
XX 22-OCT-1999; 99WO-US24747.
XX
XX 22-OCT-1998; 98US-0177315.
XX
XX (UNITW ) UNIV WASHINGTON.
XX Johnson EM, Easton R;
XX
XX WPI: 2000-339513/29.
XX
XX Truncated BAX polypeptides useful for preventing apoptosis of neurons
XX for the treatment of nervous system disorders -
XX

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PS Disclosure; Page 36-37; 43pp; English.

XX The present sequence is a mouse BAX alpha protein, a pro-apoptotic

CC protein which is a member of BCL-2 family of proteins that are involved

CC in regulation of neuronal programmed cell death. The patent discloses

CC specific truncated proteins derived from BAX alpha which inhibit neuronal

CC apoptosis induced by trophic factor deprivation. The anti-apoptotic

CC truncated BAX (tBAX) proteins include tBAX70, tBAX78 and their mutants.

CC These proteins contain the N-terminal region and at least a portion of

CC the BH3 domain of BAX alpha and lack the BH1, BH2 and C-terminal

CC transmembrane domains. The tBAX protein lacking only the

CC transmembrane domain has been shown to have anti-apoptotic activity.

CC The tBAX proteins are used to treat diseases associated with neuronal

CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,

CC spinal cord injury, head trauma and stroke.

XX

SO Sequence 192 AA;

Query Match 88.5%; Score 69; DB 21; Length 192;

Best Local Similarity 73.7%; Pred. No. 0.00012;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDGSGXXXXGGPTSSFOI 19

Db 1 MDGSGEQGSGGPTSSFOI 19

RESULT 11

AAB74122

ID AAB74122 standard; Protein; 192 AA.

XX AAB74122;

XX

DT 22-MAY-2001 (first entry)

XX

DE Murine bcl-2 associated x protein (Bax) #1.

XX

XX Murine; Bax; cytosolic; immunosuppressive; immunostimulant; infection;

KW apoptosis modulator; bcl-2 associated x protein; cancer therapy; AIDS;

KW autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;

KW myocardial infarction; traumatic brain injury; ischemia;

KW neurodegenerative diseases; hepatitis; transplant rejection; toxemia;

KW lymphoproliferative disease.

XX

OS Mus sp.

XX

XX US6184202-B1.

XX

PN 06-FEB-2001.

XX

PD 11-SEP-1997; 97US-0927326.

XX

PF 10-NOV-1994; 94US-0337646.

XX

PR 26-AUG-1993; 93US-0112208.

XX

PR 25-MAY-1994; 94US-0248819.

XX

XX (UNIV) UNIV WASHINGTON.

PA

XX Kormeyer SJ;

PI

XX WPI; 2001-256104/26.

XX

XX

PT Modulating apoptosis of a cell, useful in maintaining homeostasis in

PT adult tissues, or treating proliferative or autoimmune diseases,

PT comprises administering a bcl-2 polypeptide that interacts with a 21 kd

PT bcl-2 associated x protein

XX

XX Example 6; Fig 3; 105pp; English.

XX

XX The present invention relates to a method of modulating apoptosis of a

CC cell. The method comprises administering to the cell an agent,

CC comprising a BHL domain or BH2 domain, capable of modulating formation of

CC at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL

CC complexes, bcl-2 associated x protein (Bax):Bax complexes, bcl-2:Bax

CC complexes or bcl-XL:Bax complexes. Modulating apoptosis is especially

CC useful in cancer therapy, and treating autoimmunity, immunodeficiency

CC diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke,

CC traumatic brain injury, neurodegenerative diseases, aging, ischemia,

CC toxemia, infection, hepatitis, transplant rejection, and

CC lymphoproliferative diseases. The present sequence is murine Bax, which

XX was used in the method of the present invention.

XX

SO Sequence 192 AA;

Query Match 88.5%; Score 69; DB 22; Length 192;

Best Local Similarity 73.7%; Pred. No. 0.00012;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDGSGXXXXGGPTSSFOI 19

Db 1 MDGSGEQGSGGPTSSFOI 19

RESULT 12

AAB74125

ID AAB74125 standard; Protein; 192 AA.

XX AAB74125;

XX

DT 22-MAY-2001 (first entry)

XX

DE Murine bcl-2 associated x protein (Bax) #2.

XX

XX Murine; Bax; cytosolic; immunosuppressive; immunostimulant; infection;

KW apoptosis modulator; bcl-2 associated x protein; cancer therapy; AIDS;

KW autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;

KW myocardial infarction; traumatic brain injury; ischemia;

KW neurodegenerative diseases; hepatitis; transplant rejection; toxemia;

KW lymphoproliferative disease.

XX

OS Mus sp.

XX

XX US6184202-B1.

XX

PN 06-FEB-2001.

XX

PD 11-SEP-1997; 97US-0927326.

XX

PF 10-NOV-1994; 94US-0337646.

XX

PR 26-AUG-1993; 93US-0112208.

XX

PR 25-MAY-1994; 94US-0248819.

XX

XX (UNIV) UNIV WASHINGTON.

PA

XX Kormeyer SJ;

PI

XX WPI; 2001-256104/26.

XX

XX

PT Modulating apoptosis of a cell, useful in maintaining homeostasis in

PT adult tissues, or treating proliferative or autoimmune diseases,

PT comprises administering a bcl-2 polypeptide that interacts with a 21 kd

PT bcl-2 associated x protein

XX

XX Example 7; Fig 7; 105pp; English.

XX

XX The present invention relates to a method of modulating apoptosis of a

CC cell. The method comprises administering to the cell an agent,

CC comprising a BHL domain or BH2 domain, capable of modulating formation of

CC at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL

CC complexes, bcl-2 associated x protein (Bax):Bax complexes, bcl-2:Bax

CC complexes or bcl-XL:Bax complexes. Modulating apoptosis is especially

CC useful in cancer therapy, and treating autoimmunity, immunodeficiency

CC diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke,

CC traumatic brain injury, neurodegenerative diseases, aging, ischemia,

CC toxemia, infection, hepatitis, transplant rejection, and

CC lymphoproliferative diseases. The present sequence is murine Bax, which

CC was used in a sequence alignment in the present invention, with human Bax
CC (AAB74126), human Bcl-2 (AAB74127) and murine Bcl-2 (AAB74128).
XX

SO Sequence 192 AA:

Query Match

88.5%; Score 69; DB 22; Length 192;

Best Local Similarity 73.7%; Pred. No. 0.00012;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDGSGXXXXXGGPTSSSEQI 19

||||| |||||||||

DB 1 MDGSGEQLGSGGPTSSSEQI 19

RESULT 13

AAB35128

ID AAB35128 standard; protein; 192 AA.

AC AAB35128;

DT 03-APR-2001 (first entry)

DE Murine Bax.

KM Mouse; Bax; apoptosis modulator; BCL-2.

OS Mus sp.

PN US6165732-A.

PD 26-DEC-2000.

PF 31-JUL-1998; 98US-0127048.

PR 14-OCT-1997; 97US-0061823.

PA (UNITW) UNIV WASHINGTON.

PI Korsmeyer SJ, Schlesinger PH;

DR WPI: 2001-101692/11.

PT Identifying apoptosis-modulating compounds by contacting the compound

PT with lipid bilayer containing an ion channel formed by anti-apoptotic

PT polypeptide of Bcl-2 family and determining ion selectivity of the

PT channel -

PS Example 1; Fig 11; 34pp; English.

CC The present invention describes a method for identifying modulators of

CC apoptosis which involves contacting a compound of interest with a lipid

CC bilayer comprising a K⁺ or Cl⁻ selective channel. This channel is a

CC member of the BCL-2 family. Apoptosis modulators are also provided,

CC including Bcl-2deltaTM and BaxdeltaTM.

OY 1 MDGSGXXXXXGGPTSSSEQI 19

||||| |||||||||

ID AAU76551 standard; Protein; 192 AA.

AC AAU76551;

DT 08-MAY-2002 (first entry)

XX Murine Bax polypeptide.

KM Mouse; Bax; alpha-5 helix; alpha-6 helix; BCL-2; apoptosis modulation;

KW neoplasia; Epstein-Barr virus; African swine fever virus; adenovirus;

KW lymphoproliferative condition; cancer; arthritis; Crohn's disease; wound;

KW inflammation; autoimmune disease; immunodeficiency disease; senescence;

KW neurodegenerative disease; ischemic cell death; reperfusion cell death;

XX infertility.

OS Mus sp.

PN WO200205835-A2.

PD 24-JAN-2002.

PF 25-JUN-2001; 2001WO-US20169.

PR 17-JUL-2000; 2000US-0617878.

PA (UNITW) UNIV WASHINGTON.

PI Korsmeyer SJ, Schlesinger PH;

DR WPI: 2002-179747/23.

PT Identifying apoptosis modulating compounds for treating e.g. cancer,

PT comprises contacting a lipid membrane with a pore-forming BCL-2 member

PT and test compound, and determining if formation of large pores in the

PT membrane is regulated -

PS Example 1; Fig 11; 70pp; English.

CC The invention relates to a method for identifying apoptosis modulating

CC compounds, involving contacting a lipid membrane with a pore-forming

CC pro-apoptotic BCL-2 family member and a test compound, and determining

CC whether the compound regulates formation of large pores in the lipid

CC membrane. An increase in the number of large pores in the lipid membrane

CC indicates that the compound is an apoptosis promoter and a decrease in

CC the number of large pores indicates that it is an apoptosis inhibitor.

CC Apoptosis modulating compounds are useful for inducing or inhibiting

CC apoptosis in a cell, to treat a patient having a condition mediated by

CC excessive down-regulation of apoptosis (such as neoplasias, diseases

CC caused by Epstein-Barr virus, African swine fever virus and adenovirus,

CC lymphoproliferative conditions, cancer, arthritis, Crohn's disease,

CC inflammation and autoimmune diseases), or excessive apoptosis (such as

CC immunodeficiency diseases, senescence, neurodegenerative diseases,

CC ischemic and reperfusion cell death, infertility and wounds. This

CC sequence represents the mouse Bax polypeptide which is useful for

CC promoting apoptosis in the methods of the invention.

SO Sequence 192 AA:

Query Match 88.5%; Score 69; DB 23; Length 192;

Best Local Similarity 73.7%; Pred. No. 0.00012;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDGSGXXXXXGGPTSSSEQI 19

||||| |||||||||

DB 1 MDGSGEQLGSGGPTSSSEQI 19

RESULT 15

AAI90735

ID AAI90735 standard; peptide; 19 AA.

AC AAI90735;

DT 17-AUG-2000 (first entry)

DE Apoptotic regulation of targeting domain consensus sequence SEQ ID NO:1.

XX Apoptotic regulation of targeting domain; ART domain; BAX; apoptosis;

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2003, 12:36:33 ; Search time 24.359 Seconds
(without alignments)
160.717 Million cell updates/sec

Title: US-09-876-204-1

Perfect score: 19
Sequence: 1 MDGSGXXXXXGGPTSSSEQ1 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.podent:*
- 12: sp.virus:*
- 13: sp.vertibrate:*
- 14: sp.unclassified:*
- 15: sp.virus:*
- 16: sp.bacteriap:*
- 17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	47.4	24	08WXU1	08WXU1 homo sapien
2	9	47.4	24	08VHY7	08VHY7 mus musculu
3	9	47.4	164	09UOD6	09UOD6 homo sapien
4	9	47.4	179	09WYG7	09WYG7 homo sapien
5	6	31.6	45	09H039	09H039 homo sapien
6	6	31.6	192	08SOA3	08SOA3 felis silve
7	6	31.6	297	4 09BVV5	09BVV5 homo sapien
8	6	31.6	297	13 008107	008107 xenopus lae
9	6	31.6	312	4 09BVV3	09BVV3 homo sapien
10	6	31.6	313	12 088450	088450 sigma virus
11	6	31.6	315	17 08TIC5	08TIC5 methanosarc
12	6	31.6	364	6 028129	028129 bos taurus
13	6	31.6	411	10 09SH58	09SH58 arabidopsis
14	6	31.6	447	5 017816	017816 caenorhabdi
15	6	31.6	604	15 08Q880	08Q880 human immun
16	6	31.6	625	5 09NE37	09NE37 leishmania

17	6	31.6	625	5 09V7S1	09V7S1 drosophila
18	6	31.6	670	10 08S7H3	08S7H3 oryza sativ
19	6	31.6	740	5 09VBJ1	09VBJ1 drosophila
20	6	31.6	794	10 09SGE5	09SGE5 arabidopsis
21	6	31.6	839	10 09LMZ4	09LMZ4 arabidopsis
22	6	31.6	920	4 09P232	09P232 homo sapien
23	6	31.6	1028	11 007409	007409 mus musculu
24	6	31.6	1028	11 06Z682	06Z682 rattus norv
25	6	31.6	1148	5 017517	017517 caenorhabdi
26	6	31.6	1234	11 08VD34	08VD34 mus musculu
27	6	31.6	1576	10 041812	041812 zea mays (m
28	6	31.6	1913	5 09GRV5	09GRV5 caenorhabdi
29	6	31.6	1928	5 08T9H1	08T9H1 drosophila
30	6	31.6	2165	12 041356	041356 human respi
31	6	31.6	2165	12 P90197	P90197 human respi
32	6	31.6	2165	12 082021	082021 human respi
33	6	31.6	2165	12 041355	041355 human respi
34	6	31.6	2280	5 09VBE6	09VBE6 drosophila
35	6	31.6	2302	5 09N693	09N693 drosophila
36	6	31.6	2310	5 09GER9	09GER9 drosophila
37	6	31.6	4123	4 075851	075851 homo sapien
38	5	26.3	11	11 09R0K9	09R0K9 mus musculu
39	5	26.3	53	16 09PB22	09PB22 xyella fas
40	5	26.3	55	17 097A84	097A84 thermoplasma
41	5	26.3	59	6 095160	095160 canis famli
42	5	26.3	64	17 08TWM8	08TWM8 methanopyru
43	5	26.3	69	12 P89655	P89655 murid herpe
44	5	26.3	69	16 09KCD0	09KCD0 bacillus ba
45	5	26.3	71	10 08S522	08S522 oryza sativ

ALIGNMENTS

RESULT 1				
08WXU1 PRELIMINARY: PRT: 24 AA.				
ID	08WXU1			
AC	08WXU1			
DT	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	BCL2-associated X protein (Fragment).			
GN	BAX.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Thorntonrow E.C., Schwartzfarb E.M., Manfredi J.J.;			
RT	"A conserved intronic response element mediates direct p53-dependent			
RT	transcriptional activation of both the human and murine bax genes."			
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF339054; AAL73333.1; "			
FT	NON_TER			
FT	24			
FT	24			
SO	SEQUENCE	24 AA;	2379 MW;	8C3D3E8B7479B798 CRC64;
Query Match				
Best local similarity 100.0%; Score 9; DB 4; Length 24;				
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY 11 GGPTSSSEQ1 19				
DB 11 GGPTSSSEQ1 19				
RESULT 2				
ID	08VHY7	PRELIMINARY:	PRT:	24 AA.
AC	08VHY7			
DT	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			

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DE Bcl2-associated x protein (Fragment).
GN BAX.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC SRRAIN-BALB/C;
RA Thorborrow E.C., Schwartzfarb E.M., Manfredi J.J.;
RT "A conserved intronic response element mediates direct p53-dependent
RT transcriptional activation of both the human and murine bax genes.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF39055; AAL73334.1;
FT NON_TER
SQ SEQUENCE 24 AA; 2326 MW; 998C7E8B7479A6CC CRC64;

Query Match 47.4%; Score 9; DB 11; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPTSSDOI 19
Db 11 GGPTSSDOI 19

RESULT 3
Q9UOD6 PRELIMINARY; PRT; 164 AA.
AC Q9UOD6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Bax epsilon.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=99120940; PubMed=9920818;
RA Shi B., Triebel D., Kajiji S., Iwata K.K., Bruskini A., Mahajna J.;
RT "Identification and characterization of baxepsilon, a novel bax
RT variant missing the BH2 and the transmembrane domains.";
RL Biochem. Biophys. Res. Commun. 254:779-785(1999).
DR EMBL; AF007826; AAD22706.1;
DR InterPro; IPR000712; BCL2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01259; BH3; 1.
SQ SEQUENCE 164 AA; 18129 MW; 12CCDB8073EF4C9E CRC64;

Query Match 47.4%; Score 9; DB 4; Length 164;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPTSSDOI 19
Db 11 GGPTSSDOI 19

RESULT 4
Q9NYG7 PRELIMINARY; PRT; 179 AA.
AC Q9NYG7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Bax-sigma.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20237095; PubMed=10772918;
RA Schmitt E., Paquet C., Beauchemin M., Dever-Bertrand J., Bertrand R.;
RT "Characterization of bax-sigma, a cell death-inducing isoform of
RT Bax.";
RL Biochem. Biophys. Res. Commun. 270:868-879(2000).
DR EMBL; AF247393; AAF71267.1;
DR HSSP; Q07817; IMAZ.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR SMART; SM00337; BCL; 1.
DR PROSITE; PSS0062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01259; BH3; 1.
SQ SEQUENCE 179 AA; 19718 MW; 5802B0AC73B2E4CE CRC64;

Query Match 47.4%; Score 9; DB 4; Length 179;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GGPTSSDOI 19
Db 11 GGPTSSDOI 19

RESULT 5
Q9H039 PRELIMINARY; PRT; 45 AA.
AC Q9H039;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Hypothetical 5.1 kDa protein (Fragment).
GN DKF2P547M114.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Bloecher H., Boecher M., Brandt P., Meyes H.W., Weil B., Wiemann S.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL512746; CAC21671.1;
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 45 AA; 5069 MW; 64557BA7DB929EB7 CRC64;

Query Match 31.6%; Score 6; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TSSDOI 19
Db 1 TSSDOI 6

RESULT 6
Q8SQ43 PRELIMINARY; PRT; 192 AA.
AC Q8SQ43;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Bax-protein.
GN BAX.
OS Felis silvestris catus (Cat).

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```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamazaki J., Oguma K., Kano R., Hasegawa A.;
RT "Molecular cloning of feline bcl-2 family.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
SR EMBL: AB080724; BAB5810.1; -; 852D271AEB6923FB CRC64;
SQ SEQUENCE 192 AA; 21283 MW; 852D271AEB6923FB CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 6; Length 192;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 TSSEQ1 19
DB 14 TSSEQ1 19

RESULT 7
O9BV5 PRELIMINARY; PRT; 297 AA.
ID O9BV5;
AC O9BV5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 33.3 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC000902; AA00902.1; -;
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR001012; UBX.
DR Pfam: PF00627; UBA; 1.
DR Pfam: PF00789; UBX; 1.
DR SMART: SM00165; UBA; 1.
DR SMART: SM00166; UBX; 1.
KW Hypothetical protein.
SQ SEQUENCE 297 AA; 33325 MW; E4E0C8BBAC93F2BB CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 4; Length 297;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 PTSSEQ 18
DB 64 PTSSEQ 69

RESULT 8
O08107 PRELIMINARY; PRT; 297 AA.
ID O08107;
AC O08107;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Interphotoreceptor retinoid-binding protein (fragment).
CN IRBP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93366942; PubMed=8360278;
```

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RA Gonzalez-Fernandez F., Kittredge K.L., Rayborn M.E., Hollyfield J.G.,
RA Landers R.A., Saha M., Grainger R.M.;
RT "Interphotoreceptor retinoid-binding protein (IRBP) a major 124 kDa
RT glycoprotein in the interphotoreceptor matrix of Xenopus laevis
RT Characterization, molecular cloning, and biosynthesis.";
RL J. Cell Sci. 105:7-21(1993).
DR EMBL: X69469; CA94228.1; -;
DR InterPro: IPR003581; TSPC.
DR Pfam: PF02692; IRBP; 1.
DR SMART: SM00245; TSPC; 1.
KW Receptor.
FT NON TER
SQ SEQUENCE 297 AA; 33107 MW; 0642EAB62E16759B CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 13; Length 297;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GGPTSS 16
DB 145 GGPTSS 150

RESULT 9
O9BV93 PRELIMINARY; PRT; 312 AA.
ID O9BV93;
AC O9BV93;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to ORF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC001372; AA01372.1; -;
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR001012; UBX.
DR Pfam: PF00627; UBA; 1.
DR Pfam: PF00789; UBX; 1.
DR SMART: SM00165; UBA; 1.
DR SMART: SM00166; UBX; 1.
SQ SEQUENCE 312 AA; 35107 MW; 75C94CB67C03EB78 CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 4; Length 312;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 PTSSEQ 18
DB 64 PTSSEQ 69

RESULT 10
O08450 PRELIMINARY; PRT; 313 AA.
ID O08450;
AC O08450;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE RNA polymerase alpha subunit (EC 2.7.7.48) (Nonstructural
DE phosphoprotein).
CN P.
OS Sigma virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; unclassified Rhabdoviridae.
OX NCBI_TaxID=11301;
RN [1]
```

RP SEQUENCE FROM N.A.
 RA MDL:LINE-96074506; PubMed-7491755;
 RX Landes-Devauchelle C., Brias F., Dezelee S., Teninges D.;
 RT "gene 2 of the sigma rhabdovirus genome encodes the P protein, and
 RT gene 3 encodes a protein related to the reverse transcriptase of
 RT retroelements.";
 RL Virology 213:300-312(1995).
 DR EMBL: X91062; CAA62514.1; -
 DR FlyBase: FBgn0015810; Sigma-Virus\p.
 KW Transferrase: RNA-directed RNA polymerase; Phosphorylation;
 KW Nonstructural protein.
 SQ SEQUENCE 313 AA; 35247 MW; 8C5484FED2038E3F CRC64;

Query Match 31.6%; Score 6; DB 12; Length 313;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 PTSSEQ 18
 DB 222 PTSSEQ 227

RESULT 11

ID 08TIC5 PRELIMINARY; PRT; 315 AA.
 AC 08TIC5;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DE Predicted protein.
 GN MA4230.
 OS Methanosarcina acetivorans.
 OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID-2214;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;
 RX MDL:LINE-21929760; PubMed-11932238;
 RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Althor D., Brown A.,
 RA Allen N., Navlor J., Stange-Thomann N., Dearellano K., Johnson R.,
 RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
 RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
 RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
 RA Springer T.A., Umeyam L.A., White O., White R.H., de Macario E.C.,
 RA Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
 RA Pritchett M., Sowatz K.R., Swanson R.V., Zinder S.H., Lander E.,
 RA Metcalf W.W., Birken B.;
 RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
 RT and physiological diversity.";
 RL Genome Res. 12:532-542(2002).
 DR EMBL: AE011334; AA07575.1; -
 KW Complete proteome.
 SQ SEQUENCE 315 AA; 34004 MW; 3649A8CBE8784486 CRC64;

Query Match 31.6%; Score 6; DB 17; Length 315;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GGPTSS 16
 DB 257 GGPTSS 262

RESULT 12

ID 028129 PRELIMINARY; PRT; 364 AA.
 AC 028129;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE Interstitial retinol binding protein (IRBP) (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID-9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MDL:LINE-87293907; PubMed-3617506;
 RA Liou G.T., Fong S.-L., Beattie W.G., Cook R.G., Leone J.,
 RA Landers R.A., Alvarez R.A., Wang C., Li Y., Bridges C.D.B.;
 RT "Bovine interstitial retinol-binding protein (IRBP)-isolation and
 RT sequence analysis of cDNA clones, characterization and in vitro
 RT translation of mRNA.";
 RL Vision Res. 26:1645-1653(1986).
 DR EMBL: M19390; AAA30592.1; -
 DR InterPro: IPR003581; TSPC.
 DR Pfam: PF02692; IRBP; 1.
 DR SMART: SM00245; TSPC; 1.
 FT NON_TER 1

SQ SEQUENCE 364 AA; 39621 MW; 8F0914CA142C5353 CRC64;

Query Match 31.6%; Score 6; DB 6; Length 364;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GGPTSS 16
 DB 162 GGPTSS 167

RESULT 13

ID 09SH58 PRELIMINARY; PRT; 411 AA.
 AC 09SH58;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE F22C12.16.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID-3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Khan S., Brooks S., Buehler E., Chao O., Dunn P., Kim C.,
 RA Walker M., Altati H., Araujo R., Conn L., Conway A.B., Gonzalez A.,
 RA Hansen N.F., Hulzar L., Kremetska I., Lenz C., Li J., Liu S.,
 RA Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G.,
 RA Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC F22C12 from chromosome
 RT 1";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC007764; AF24565.1; -
 SQ SEQUENCE 411 AA; 44511 MW; DA4EFD73C5D7797D CRC64;

Query Match 31.6%; Score 6; DB 10; Length 411;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 PTSSEQ 18
 DB 134 PTSSEQ 139

RESULT 14

ID 017816 PRELIMINARY; PRT; 447 AA.
 AC 017816;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE C08B6.4 protein.
 GN C08B6.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilkinson J;
 RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL; 272502; CAA96587.1; -.
 DR HSSP; P23951; 2BAA.
 DR InterPro: IPR000726; Glyco_hydro_19.
 DR Pfam: PF00182; Glyco_hydro_19; 1.
 DR ProDom: PD000574; Glyco_hydro_19; 1.
 SQ SEQUENCE 447 AA; 49583 MW; 6B4EC67A89B13D17 CRC64;

Query Match 31.6%; Score 6; DB 5; Length 447;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSS 16
 |||||
 Db 166 GGPTSS 171

RESULT 15
 Q80880
 ID Q80880 PRELIMINARY; PRT; 604 AA.
 AC Q80880;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Pol protein (Fragment).
 GN POL.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=00GAB-10K;
 RA Vergne I., Mitsoul I., Malonga-Mouelet G., Mavoungou R., Mansaray H.,
 RA Peeters M., Delaporte E.;
 RT "Emergence of HIV-1 drug-resistant variants in Gabon: need for
 RT implementation of guidelines on ARV use and drug resistance monitoring
 RT in developing countries.";
 RL J. Acquir. Immune Defic. Syndr. 0:0-0(2002).
 DR EMBL; AJ313412; CAC86073.1; -.
 FT NON_TER 1
 FT NON_TER 1
 FT NON_TER 604
 SQ SEQUENCE 604 AA; 68931 MW; BB07C9B6D30C4E62 CRC64;

Query Match 31.6%; Score 6; DB 15; Length 604;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PTSSSEQ 18
 |||||
 Db 25 PTSSSEQ 30

Search completed: January 7, 2003, 12:39:49
 Job time : 26.359 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:31:53 ; Search time 6.82051 Seconds
(without alignments)
115.541 Million cell updates/sec

Title: US-09-876-204-1

Perfect score: 19
Sequence: 1 MDGSGXXXXGPTSSSEQI 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	47.4	143	1	BAXD_HUMAN
2	9	47.4	192	1	BAXA_BOVIN
3	9	47.4	192	1	BAXA_HUMAN
4	9	47.4	192	1	BAXA_MOUSE
5	9	47.4	192	1	BAXA_RAT
6	9	47.4	218	1	BAXB_HUMAN
7	6	31.6	105	1	YGRM_MICRO
8	6	31.6	298	1	Y3JK_HUMAN
9	6	31.6	337	1	FSA_SHEEP
10	6	31.6	344	1	FSA_BOVIN
11	6	31.6	344	1	FSA_HORSE
12	6	31.6	344	1	FSA_PIG
13	6	31.6	680	1	YPR1_YEAST
14	6	31.6	790	1	DNL1_ARATH
15	6	31.6	1247	1	IRBP_HUMAN
16	6	31.6	1285	1	IRBP_BOVIN
17	6	31.6	2165	1	RREL_HRSVA
18	6	31.6	2245	1	MYSU_DICDI
19	5	26.3	41	1	BAXC_HUMAN
20	5	26.3	172	1	CATR_NAEGR
21	5	26.3	183	1	RS10_ORYSA
22	5	26.3	184	1	RLI3_SCHMA
23	5	26.3	191	1	RNH2_CAMJE
24	5	26.3	194	1	CSF3_FELCA
25	5	26.3	198	1	YH13_YEAST
26	5	26.3	201	1	YMBD_YEAST
27	5	26.3	211	1	ACD2_LISIN
28	5	26.3	211	1	ACD2_LISMO
29	5	26.3	223	1	YHDI_YEAST
30	5	26.3	227	1	CIS3_YEAST
31	5	26.3	234	1	PVG_CYACA
32	5	26.3	255	1	MYFS_HUMAN
33	5	26.3	256	1	USO2_PRVN3

34	5	26.3	258	1	HY1_ECOLI	P30147 escherichia
35	5	26.3	268	1	TRYP_STRGCA	O54179 streptomyces
36	5	26.3	272	1	ERG_MOUSE	P81270 mus musculus
37	5	26.3	274	1	CCG8_NEUCR	O01306 neurospora
38	5	26.3	285	1	STAR_PIG	O28596 sus scrofa
39	5	26.3	303	1	PANE_YERPE	O82551 yersinia pe
40	5	26.3	309	1	YAY4_SCHPO	O10212 schizosacch
41	5	26.3	312	1	RHAR_ECOLI	P09378 escherichia
42	5	26.3	314	1	LEDO_SALTY	P46924 salmonella
43	5	26.3	320	1	CELL_AGABI	O00023 agaricus bi
44	5	26.3	322	1	GDC_RAT	P16261 rattus norv
45	5	26.3	323	1	PREA_CYACA	O91151 cyanidium c

ALIGNMENTS

RESULT 1					
ID	BAXD_HUMAN	STANDARD:	PRT:	143 AA.	
AC	P55269;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	BAX protein, cytoplasmic isoform delta.				
CN	BAX.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=95331797; PubMed=7607685;				
RA	Apte S.S., Mattei M.-G., Olsen B.R.;				
RT	"Mapping of the human BAX gene to chromosome 19q13.3-q13.4 and				
RT	isolation of a novel alternatively spliced transcript, BAX delta.";				
RL	Genomics 26:592-594(1995).				
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).				
CC	-1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE				
CC	CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY				
CC	ALTERNATIVE SPLICING.				
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.				
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.				
CC	-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.				
CC					
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CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC					
CC	EMBL: U19599; AAC50142.1; -				
CC	GeneW: HGNC:959; BAX.				
CC	MIM: 600040; -				
DR	InterPro: IPR002475; BCL2_family.				
DR	InterPro: IPR000712; Bcl2_BH.				
DR	Pfam: PF00452; Bcl-2; 1.				
DR	SMART: SM00337; BCL; 1.				
DR	PROSITE: PS01080; BH1; 1.				
DR	PROSITE: PS01258; BH2; 1.				
DR	PROSITE: PS50062; BCL2_FAMILY; 1.				
KW	Apoptosis; Alternative splicing.				
FT	DOMAIN 49				
FT	DOMAIN 101				
FT	DOMAIN 116				
SO	SEQUENCE 143 AA; 15772 MW; BADF4D71D06A75AB CRC64;				
Query Match					
Best Local Similarity 47.4%; Score 9; DB 1; Length 143;					
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OY	11	GGPTSSSEQI 19			

Db 11 GGPSSSEQI 19

Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

BAXA_BOVIN STANDARD; PRT; 192 AA.

ID BAXA_BOVIN

002703;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Apoptosis regulator BAX, membrane isoform alpha.

GN BAX.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovine; Bos.

OX NCBI_Taxid=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-Holstein; TISSUE=Thymus;

RX MEDLINE=98162580; PubMed=9501056;

RA Reyes R.A., Cockerell G.L.,

RT "Increased ratio of bcl-2/bax expression is associated with bovine

leukemia virus-induced leukemogenesis in cattle."

RL Virology 242:184-192(1998).

CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND

ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS

HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,

ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY

LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE

CESSATION OF SPERM PRODUCTION (BY SIMILARITY).

CC SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,

E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1 (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Membrane-bound (BY SIMILARITY).

CC -1- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO

CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE

SPLICING.

CC -1- DOMAIN: INTRACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND

BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION

WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.

CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

CC -----

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or send an email to license@isb-sib.ch).

CC -----

DR EMBL: U92569; AAC48806.1; --

DR HSP: Q07817; 1MAZ.

DR InterPro: IPR002475; BCL2_family.

DR InterPro: IPR000712; BCL2_BH.

DR Pfam: PF00452; Bcl-2; 1.

DR SMART: SMO0337; BCL.1.

DR PROSITE: PS01080; BH1.1.

DR PROSITE: PS01258; BH2.1.

DR PROSITE: PS01259; BH3.1.

DR PROSITE: PS0062; BCL2_FAMILY.1.

KW Apoptosis; Transmembrane; Alternative splicing.

FT DOMAIN 59 73 BH3.

FT DOMAIN 98 118 BH1.

FT DOMAIN 150 165 BH2.

FT TRANSMEM 172 192 POTENTIAL.

SO SEQUENCE 192 AA; 21259 MW; 6B4D5BBAF1D5F87E CRC64;

Query Match 47.4%; Score 9; DB 1; Length 192;

OY 11 GGPSSSEQI 19

Db 11 GGPSSSEQI 19

RESULT 3

BAXA_HUMAN STANDARD; PRT; 192 AA.

ID BAXA_HUMAN

007812;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Apoptosis regulator BAX, membrane isoform alpha.

GN BAX.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=B-cell;

RX MEDLINE=93364978; PubMed=8358790;

RA Oliva Z.N., Millman C.L., Korsmeyer S.J.;

RT "bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that

accelerates programmed cell death."

RL Cell 74:609-619(1993).

RN [2]

RP MUTAGENESIS, AND FUNCTION OF BH3 DOMAIN.

RX MEDLINE=96091131; PubMed=8521816;

RA Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.;

RT "A conserved domain in Bax, distinct from BH1 and BH2, mediates cell

death and protein binding functions."

RL EMBO J. 14:5589-5596(1995).

RN [3]

RP VARIANT PLASMACYTOMA GLU-11, VARIANT T-CELL ACUTE LYMPHOBLASTIC

LEUKEMIA ARG-67, AND VARIANT BURKITT LYMPHOMA VAL-108.

RX MEDLINE=98200607; PubMed=9531611;

RA Meljertink J.P.P., Mensink E.J.B.W., Wang K., Sedlak T.W.,

RT "Hematopoietic malignancies demonstrate loss-of-function mutations of

BAX."

RL Blood 91:2991-2997(1998).

CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND

ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS

HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,

ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.

CC SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,

E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.

CC -1- SUBCELLULAR LOCATION: Membrane-bound.

CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE

CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY

ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.

CC -1- DOMAIN: INTRACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND

BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION

WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

CC -1- DISEASE: Defects in BAX are found in some cell lines from

hematopoietic malignancies as T-cell acute lymphoblastic leukemia,

Burkitt lymphoma, and plasmacytoma.

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.

CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

CC -----

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL: L22473; AAA03619.1; -
CC PIR: A47538; A47538.
CC HSSP: 007817; 1MAZ.
CC Genew: HGNC:959; BAX.
CC MIM: 600040; -
CC InterPro: IPR002475; BCL2_family.
CC InterPro: IPR000712; Bcl2_BH.
CC Pfam: PF00452; BCL-2; 1.
CC SMART: SM00337; BCL; 1.
CC PROSITE: PS50062; BCL2_FAMILY; 1.
CC PROSITE: PS01080; BH1; 1.
CC PROSITE: PS01258; BH2; 1.
CC PROSITE: PS01259; BH3; 1.
CC Apoptosis: Anti-oncogene; Transmembrane; Alternative splicing;
CC Disease mutation.
CC DOMAIN 59 73 BH3.
CC FT DOMAIN 98 118 BH1.
CC FT DOMAIN 150 165 BH2.
CC TRANSMEM 172 192 POTENTIAL.
CC VARIANT 11 11 G -> E (IN PLASMACYTOMA).
CC VARIANT 67 67 G -> R (IN T-CELL ACUTE LYMPHOBLASTIC
CC LEUKEMIA; LOSS OF HETERODIMERIZATION WITH
CC BCL-2 OR BCL-X(L)).
CC FT VARIANT 108 108 /FTID-VAR_007809.
CC FT VARIANT 108 108 G -> V (IN BURKITT LYMPHOMA; LOSS OF
CC HOMODIMERIZATION).
CC FT VARIANT 108 108 /FTID-VAR_013576.
CC SQ SEQUENCE 192 AA; 21184 MW; 6C0CDB0A7DEB4994 CRC64;

Query Match 47.4%; Score 9; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
DB 11 GGPTSSEQI 19

RESULT 4
BAXA_MOUSE
ID BAXA_MOUSE STANDARD: PRT; 192 AA.
AC 007813;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X DBA/2;
RX MEDLINE=93364978; PubMed=8358790;
RA Oliva J.N., Millman C.L., Korsmeyer S.J.;
RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
RT accelerates programmed cell death.";
RL Cell 74:609-619(1993).
CC -I- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
CC HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY
CC LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE
CC CESSATION OF SPERM PRODUCTION.
CC -I- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC -I- SUBCELLULAR LOCATION: Membrane-bound.

CC -I- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO
CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
CC SPLICING.
CC -I- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC -I- DOMAIN: INTACT BH DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC EMBL: L22472; AAA03622.1; -
CC CC
CC HSSP: P53563; 1AF3.
CC MGD: MGI:99702; Bax.
CC DR InterPro: IPR002475; BCL2_family.
CC DR InterPro: IPR000712; Bcl2_BH.
CC Pfam: PF00452; BCL-2; 1.
CC SMART: SM00337; BCL; 1.
CC PROSITE: PS01080; BH1; 1.
CC PROSITE: PS01258; BH2; 1.
CC PROSITE: PS01259; BH3; 1.
CC PROSITE: PS50062; BCL2_FAMILY; 1.
CC Apoptosis; Transmembrane; Alternative splicing.
CC FT DOMAIN 59 73 BH3.
CC FT DOMAIN 98 118 BH1.
CC FT DOMAIN 150 165 BH2.
CC TRANSMEM 172 192 POTENTIAL.
CC SQ SEQUENCE 192 AA; 21394 MW; D2E0B356579FAFF CRC64;

Query Match 47.4%; Score 9; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
DB 11 GGPTSSEQI 19

RESULT 5
BAXA_RAT
ID BAXA_RAT STANDARD: PRT; 192 AA.
AC 063690; 062995; 064383;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96178771; PubMed=8600029;
RA Han J., Sabbatini P., Perez D., Rao L., Modha D., White E.;
RT "The E1B 19K protein blocks apoptosis by interacting with and
RT inhibiting the p53-inducible and death-promoting Bax protein.";
RL Genes Dev. 10:461-477(1996).
RN [2]
RP SEQUENCE OF 75-192 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97147318; PubMed=8994223;
RA Madison D.L., Pfeiffer S.E.;

RT "Cloning of the 3' end of rat bax-alpha and corresponding
RT developmental down-regulation in differentiating primary, cultured
RT oligodendrocytes."
RL Neurosci. Lett. 220:183-186(1996).
RN [3]
RP SEQUENCE OF 37-169 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Ovary;
RX MEDLINE=95129487; PubMed=7828536;
RA Tilly J.L., Tilly K.L., Kenton M.L., Johnson A.L.;
RT "Expression of members of the bcl-2 gene family in the immature rat
RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT cell apoptosis is associated with decreased bax and constitutive
RT bcl-2 and bcl-x-long messenger ribonucleic acid levels."
RL Endocrinology 136:232-241(1995).
CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
CC HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC -1- SUBCELLULAR LOCATION: Membrane-bound.
CC -1- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO
CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES. WITH
CC HIGHEST LEVELS IN THE TESTIS AND OVARY.
CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL: U49729; AAC26327.1; -
DR EMBL: U59184; AAC52998.1; -
DR EMBL: U32098; AAA75200.1; -
DR EMBL: S76511; AAC60700.2; -
DR HSSP: P53563; IAF3.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL_1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
KW Apoptosis; Transmembrane; Alternative splicing.
FT DOMAIN 59 73 BH3.
FT DOMAIN 98 118 BH1.
FT DOMAIN 150 165 BH2.
FT TRANSMEM 172 192 POTENTIAL.
FT CONFLICT 72 72 S->N (IN REF. 3).
FT CONFLICT 76 76 L->M (IN REF. 2).
FT CONFLICT 126 126 C->Y (IN REF. 2).
FT CONFLICT 149 149 L->F (IN REF. 3).
FT CONFLICT 159 159 D->E (IN REF. 1).
SQ SEQUENCE 192 AA; 21350 MW; 7B3CD198D56DF589 CRC64;

Query Match 47.4%; Score 9; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 GGPSSSEQI 19
|||||||
RESULT 6
BAXB_HUMAN STANDARD; PRT; 218 AA.
ID BAXB_HUMAN
AC Q07814;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator BAX, cytoplasmic isoform beta.
GN BAX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=93364978; PubMed=8358790;
RA Oliveira Z.N., Millman C.L., Korsmeyer S.J.;
RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
RT accelerates programmed cell death."
RL Cell 74:609-619(1993).
CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
CC HOMOLOG E1B 19K PROTEIN.
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: I22474; AAA03620.1; -
DR PIR: B47538; B47538.
DR HSSP: Q07817; IMA2.
DR Genew: HGNC:959; BAX.
DR MIM: 600040; -
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL_1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
KW Apoptosis; Alternative splicing.
FT DOMAIN 59 73 BH3.
FT DOMAIN 98 118 BH1.
FT DOMAIN 150 165 BH2.
SQ SEQUENCE 218 AA; 24220 MW; F69DCD70F960192F CRC64;

Query Match 47.4%; Score 9; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.0046;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GGPTSSRQI 19
 |||||
 Db 11 GGPTSSRQI 19

RESULT 7

YGRM_MICRO

ID YGRM_MICRO STANDARD: PRT; 105 AA.

AC P24621;

DT 01-MAR-1992 (Rel. 21, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein in GRM 3'region (Fragment).

OS Micromonospora rosea.

OC Bacteria; Actinobacteriales; Actinobacteria (class); Actinobacteridae;

OC Actinomycetales; Micromonosporinae; Micromonosporaceae;

OC Micromonospora.

OX NCBI_TaxID=1878;

RN (1);

RP SEQUENCE FROM N.A.

RX MEDLINE=91192615; PubMed=2013410;

RA Kelemen G.H., Cundliffe E., Fiancsek I.;

RT "Cloning and characterization of gentamicin-resistance genes from

RT Micromonospora purpurea and Micromonospora rosea.";

RL Gene 98:53-60(1991).

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CC -----

CC EMBL: M5521; AAA25339.1; -.

DR PIR: PM0018; PM0018.

KM Antibiotic resistance: Hypothetical protein.

FT NON_TER 105

SQ SEQUENCE 105 AA; 11112 MW; 56125793440BA48C CRC64;

Query Match 31.6%; Score 6; DB 1; Length 105;

Best Local Similarity 100.0%; Pred. No. 4.1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSS 16
|||||

Db 81 GGPTSS 86

RESULT 8

Y33K_HUMAN

ID Y33K_HUMAN STANDARD: PRT; 298 AA.

AC Q04323;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical 33.4 kDa protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.

OX NCBI_TaxID=9606;

RN (1);

RP SEQUENCE FROM N.A.

RA Pollard K.M.;

RL Submitted (JUN-1991) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 1 UBA DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 UBX DOMAIN.

CC -----

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CC -----

CC EMBL: M68864; AAA36396.1; -.

DR InterPro: IPR000449; UBA_domain.

DR InterPro: IPR001012; UBX.

DR Pfam: PF00627; UBA; 1.

DR Pfam: PF00789; UBX; 1.

DR SMART: SM00165; UBA; 1.

DR SMART: SM00166; UBX; 1.

KW Hypothetical protein.

SQ SEQUENCE 298 AA; 33396 MW; 6C671CFF4AC15D7 CRC64;

Query Match 31.6%; Score 6; DB 1; Length 298;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PTSSRQ 18
|||||

Db 64 PTSSRQ 69

RESULT 9

FSA_SHEEP

ID FSA_SHEEP STANDARD: PRT; 337 AA.

AC P31514;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Follistatin precursor (Fst) (Activin-binding protein) (Fragment).

GN FST.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Ovis.

OX NCBI_TaxID=9940;

RN (1);

RP SEQUENCE FROM N.A.

RX MEDLINE=92337809; PubMed=1632897;

RA Tisdall D.J., Hill D., Petersen G.B., Fleming J.S.;

RT "Ovine follistatin: characterization of cDNA and expression in sheep

RT ovary during the luteal phase of the oestrous cycle.";

RL J. Mol. Endocrinol. 8:258-264(1992).

CC -1- FUNCTION: BINDS DIRECTLY TO ACTIVIN AND FUNCTIONS AS AN ACTIVIN

CC ANTAGONIST. SPECIFIC INHIBITOR OF THE BIOSYNTHESIS AND SECRETION

CC OF PITUITARY FOLLICLE STIMULATING HORMONE (FSH).

CC -1- SUBUNIT: MONOMER (POTENTIAL).

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: CONTAINS 3 FOLLISTATIN-LIKE DOMAINS.

CC -1- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.

CC -----

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CC -----

CC EMBL: M63123; AAA31522.1; -.

DR HSP: P37109; 1PCF.

DR InterPro: IPR003645; FOIN.

DR InterPro: IPR002350; Kazal.

DR Pfam: PF00050; Kazal; 3.

DR SMART: SM00274; FOLN; 3.

DR SMART: SM00280; KAZAL; 3.

DR PROSITE: PS00282; KAZAL; FALSE_NEG.

KW Glycoprotein; Repeat; Signal.

FT NON_TER 1

FT SIGNAL <1 22

FT CHAIN 23 337 FOLLISTATIN.

FT DOMAIN 87 110 FOLLISTATIN 1.
FT DOMAIN 111 157 KAZAL-LIKE 1.
FT DOMAIN 160 183 FOLLISTATIN 2.
FT DOMAIN 185 232 KAZAL-LIKE 2.
FT DOMAIN 237 261 FOLLISTATIN 3.
FT DOMAIN 263 309 KAZAL-LIKE 3.
FT DOMAIN 314 326 ASP/GLU-RICH (HIGHLY ACIDIC).
FT DISULFID 111 143 BY SIMILARITY.
FT DISULFID 115 136 BY SIMILARITY.
FT DISULFID 125 157 BY SIMILARITY.
FT DISULFID 185 218 BY SIMILARITY.
FT DISULFID 189 232 BY SIMILARITY.
FT DISULFID 200 232 BY SIMILARITY.
FT DISULFID 263 295 BY SIMILARITY.
FT DISULFID 267 288 BY SIMILARITY.
FT DISULFID 277 309 BY SIMILARITY.
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 337 AA; 37082 MW; 1E8BE1BB6B109C4 CRC64;

Query Match 31.6%; Score 6; DB 1; Length 337;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PTSSEQ 18
Db 192 PTSSEQ 197

RESULT 10
FSA_BOVIN STANDARD; PRT; 344 AA.

ID FSA_BOVIN STANDARD; PRT; 344 AA.
AC P50291;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Follistatin precursor (FS) (Activin-binding protein).
GN FST.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Holstein; TISSUE=Testicle; and Ovary;
RX MEDLINE=9428084; PubMed=801323;
RA Houde A., Lusler J.G., Echier J.F., Gagnon C., Silversides D.W.,
RT "Cloning and tissue expression of bovine Follistatin cDNA.",
RL Mol. Reprod. Dev. 37:391-397(1994).
CC -1- FUNCTION: BINDS DIRECTLY TO ACTIVIN AND FUNCTIONS AS AN ACTIVIN
ANTAGONIST. SPECIFIC INHIBITOR OF THE BIOSYNTHESIS AND SECRETION
OF PITUITARY FOLLICLE STIMULATING HORMONE (FSH).
CC -1- SUBUNIT: MONOMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: CONTAINS 3 FOLLISTATIN-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
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CC
DR EMBL; L21716; AAA30522.1; -
DR HSSP; P37109; IPCE.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR002350; KAZAL.
DR Pfam; PF000050; KAZAL; 3.
DR SMART; SM00274; FOLN; 3.
DR SMART; SM00280; KAZAL; 3.

DR PROSITE; PS00282; KAZAL; FALSE_NEG.
KW Glycoprotein; Repeat; Signal.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 344 FOLLISTATIN.
FT DOMAIN 94 117 FOLLISTATIN 1.
FT DOMAIN 118 164 KAZAL-LIKE 1.
FT DOMAIN 167 190 FOLLISTATIN 2.
FT DOMAIN 192 239 KAZAL-LIKE 2.
FT DOMAIN 244 268 FOLLISTATIN 3.
FT DOMAIN 270 316 KAZAL-LIKE 3.
FT DISULFID 118 150 BY SIMILARITY.
FT DISULFID 122 143 BY SIMILARITY.
FT DISULFID 132 164 BY SIMILARITY.
FT DISULFID 192 225 BY SIMILARITY.
FT DISULFID 196 218 BY SIMILARITY.
FT DISULFID 207 239 BY SIMILARITY.
FT DISULFID 270 302 BY SIMILARITY.
FT DISULFID 274 295 BY SIMILARITY.
FT DISULFID 284 316 BY SIMILARITY.
FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 344 AA; 37959 MW; 018FEE8A84F87710 CRC64;

Query Match 31.6%; Score 6; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PTSSEQ 18
Db 199 PTSSEQ 204

RESULT 11
FSA_HORSE STANDARD; PRT; 344 AA.

ID FSA_HORSE STANDARD; PRT; 344 AA.
AC O62650;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Follistatin precursor (FS) (Activin-binding protein).
GN FST.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_Taxid=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Follicle;
RX MEDLINE=99261574; PubMed=10331189;
RA Sugawara Y., Yamanouchi K., Naito K., Tachi C., Tojo H., Sawasaki T.,
RT "Molecular cloning of cDNA for equine follistatin and its gene
expression in the reproductive tissues of the mare.",
RL J. Vet. Med. Sci. 61:201-207(1999).
CC -1- FUNCTION: BINDS DIRECTLY TO ACTIVIN AND FUNCTIONS AS AN ACTIVIN
ANTAGONIST. SPECIFIC INHIBITOR OF THE BIOSYNTHESIS AND SECRETION
OF PITUITARY FOLLICLE STIMULATING HORMONE (FSH).
CC -1- SUBUNIT: MONOMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 FOLLISTATIN-LIKE DOMAINS.
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CC
DR EMBL; AB010829; BAA25699.1; -
DR HSSP; P37109; IPCE.
DR InterPro; IPR003645; FOLN.
DR InterPro; IPR002350; KAZAL.


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DR Pfam: PF00050; Kazal; 3.
DR SMART: SM00274; POLN; 3.
DR SMART: SM00280; KAZAL; 3.
DR PROSITE: PS00282; KAZAL; FALSE_NEG.
KW Glycoprotein; Repeat; Signal.
FT SIGNAL 1 29
FT CHAIN 30 344
FT DOMAIN 94 117
FT DOMAIN 117 164
FT DOMAIN 167 190
FT DOMAIN 192 239
FT DOMAIN 244 268
FT DOMAIN 270 316
FT DISULFID 118 150
FT DISULFID 122 143
FT DISULFID 132 164
FT DISULFID 192 225
FT DISULFID 196 218
FT DISULFID 207 239
FT DISULFID 270 302
FT DISULFID 274 295
FT DISULFID 284 316
FT CARBOHYD 124 124
FT CARBOHYD 288 288
SQ SEQUENCE 344 AA; 38002 MW; 1803577D2D9BE4AA CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 PTSSEQ 18
Db 199 PTSSEQ 204

RESULT 12
FSA_PIG STANDARD; PRT; 344 AA.
AC P10669; P10670;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Follistatin precursor (FS) (Activin-binding protein).
GN FST.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88209050; PubMed=3365249;
RA Shimasaki S., Koga M., Esch F., Mercado M., Cooksey K., Koba A.,
RA Ling N.;
RT "Porcine follistatin gene structure supports two forms of mature
RT follistatin produced by alternative splicing."
RL Biochem. Biophys. Res. Commun. 152:717-723(1988).
RN [2]
RP SEQUENCE OF 1-334 FROM N.A.
RX MEDLINE=91042571; PubMed=3153465;
RA Esch F.S., Shimasaki S., Mercado M., Cooksey K., Ling N., Ying S.,
RA Ueno N., Guillemin R.;
RT "Structural characterization of follistatin: a novel follicle-
RT stimulating hormone release-inhibiting polypeptide from the gonad."
RL Mol. Endocrinol. 1:849-855(1987).
CC -i- FUNCTION: BINDS DIRECTLY TO ACTIVIN AND FUNCTIONS AS AN ACTIVIN
CC ANTAGONIST. SPECIFIC INHIBITOR OF THE BIOSYNTHESIS AND SECRETION
CC OF PITUITARY FOLLICLE STIMULATING HORMONE (FSH).
CC -i- SUBUNIT: MONOMER (POTENTIAL).
CC -i- SUBCELLULAR LOCATION: Secreted.
CC -i- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A (SHOWN HERE) AND A'; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -i- SIMILARITY: CONTAINS 3 FOLLISTATIN-LIKE DOMAINS.
CC -i- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.

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CC -----
DR EMBL: M19529; AAA31036.1; -.
DR EMBL: M19529; AAA31037.1; -.
DR EMBL: M36512; AAA31038.1; -.
DR PIR: A27701; A27701.
DR HSSP: P37109; 1PCE.
DR InterPro: IPR003645; POLN.
DR InterPro: IPR002350; Kazal.
DR Pfam: PF00050; Kazal; 3.
DR SMART: SM00274; POLN; 3.
DR SMART: SM00280; KAZAL; 3.
DR PROSITE: PS00282; KAZAL; FALSE_NEG.
KW Glycoprotein; Repeat; Signal; Alternative splicing.
FT SIGNAL 1 29
FT CHAIN 30 344
FT DOMAIN 94 117
FT DOMAIN 117 164
FT DOMAIN 167 190
FT DOMAIN 192 239
FT DOMAIN 244 268
FT DOMAIN 270 316
FT DOMAIN 321 333
FT DISULFID 118 150
FT DISULFID 122 143
FT DISULFID 132 164
FT DISULFID 192 225
FT DISULFID 196 218
FT DISULFID 207 239
FT DISULFID 270 302
FT DISULFID 274 295
FT DISULFID 284 316
FT CARBOHYD 124 124
FT CARBOHYD 288 288
FT VARSPLIC 318 344
SQ SEQUENCE 344 AA; 38035 MW; 6906E7A23CF9BD21 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 PTSSEQ 18
Db 199 PTSSEQ 204

RESULT 13
YPK1_YEAST STANDARD; PRT; 680 AA.
ID YPK1_YEAST
AC P12688;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase YPK1 (EC 2.7.1.1.-).
GN YPK1 OR YKL126W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89090805; PubMed=2850145;
RA Maurer R.A.;
RT "Isolation of a yeast protein kinase gene by screening with a
RT mammalian protein kinase cDNA."
RL DNA 7:469-474(1988).

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RN [2]
RP SEQUENCE FROM N.A.
RA Rad M.R., Xu G., Kirchhath L., Fritz C., Keuchel H., Hollenberg C.P.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP DISCUSSION OF SEQUENCE:
RX MEDLINE=93173125; PubMed=8437590;
RA Chen P.C., Lee K.S., Levin D.E.;
RT "A pair of putative protein kinase genes (YPK1 and YPK2) is required
RL Mol. Gen. Genet. 236:443-447(1993).
CC -1- FUNCTION: PLAYS AN ESSENTIAL ROLE IN THE PROLIFERATION OF YEAST
CC CELLS.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC RAC SUBFAMILY. STRONGEST TO YPK2.
CC -----
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CC -----
DR EMBL: M21307; AAA34880.1; -
DR EMBL: Z28126; CAA81967.1; -
DR PIR: S37955; S37955.
DR HSSP: P05132; ICPK.
DR SGD: S0001609; YPK1.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR000961; Pkinase_C.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; Pkinase_1.
DR Pfam: PF00433; Pkinase_C_1.
DR Prodom: PD000001; Euk_Pkinase_1.
DR SMART: SM00133; S_TK_X_1.
DR SMART: SM00220; S_TKc_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 847 602 PROTEIN KINASE.
FT NE_BIND 853 361 ATP (BY SIMILARITY).
FT BINDING 876 376 ATP (BY SIMILARITY).
FT ACT_SITE 870 470 BY SIMILARITY.
FT CONFLICT 201 201 P -> L (IN REF. 2).
FT CONFLICT 553 553 M -> I (IN REF. 2).
SQ SEQUENCE 680 AA; 76479 MW; 00112BB849CD2B5 CRC64;

Query Match 31.6%; Score 6; DB 1; Length 680;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 TSSBOI 19
DB 137 TSSBOI 142

RESULT 14
DNL1_ARATH STANDARD: PRT; 790 AA.
AC Q42572;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE DNA ligase (EC 6.5.1.1) [polydeoxyribonucleotide synthase (ATP)].
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=98346005; PubMed=9681027;
RA Taylor R.M., Hamer M.J., Rosamond J., Bray C.M.;
RT "Molecular cloning and functional analysis of the Arabidopsis
RL thaliana DNA ligase I homologue.";
RL Plant J. 14:75-81(1998).
CC -1- FUNCTION: THIS PROTEIN SEALS DURING DNA REPLICATION, DNA
CC RECOMBINATION AND DNA REPAIR NICKS IN DOUBLE-STRANDED DNA.
CC -1- CATALYTIC ACTIVITY: ATP + [deoxyribonucleotide](N) +
CC [deoxyribonucleotide](N+M) ->
CC [deoxyribonucleotide](N+M).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X97924; CAA6599.1; -
DR InterPro: IPR000977; DNA_Ligase.
DR Pfam: PF01068; DNA_Ligase_1.
DR TIGRFAMS: TIGR00574; dnll_1.
DR PROSITE: PS00697; DNA_LIGASE_A1_1.
DR PROSITE: PS00333; DNA_LIGASE_A2_1.
DR PROSITE: PS0160; DNA_LIGASE_A3_1.
KW Ligase; DNA repair; DNA replication; DNA recombination; Cell division;
KW ATP-binding.
FT BINDING 444 444 AMP (BY SIMILARITY).
SQ SEQUENCE 790 AA; 87766 MW; 2CEE18CBA9D5C224 CRC64;

Query Match 31.6%; Score 6; DB 1; Length 790;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 TSSBOI 19
DB 764 TSSBOI 769

RESULT 15
IRBP_HUMAN STANDARD: PRT; 1247 AA.
ID IRBP_HUMAN
AC P10745;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interphotoreceptor retinoid-binding protein precursor (IRBP)
DE (Interstitial retinol-binding protein).
GN RBP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89255256; PubMed=2542268;
RA Liou G.I., Ma D.-P., Yang Y.-W., Geng L., Zhu C., Baehr W.;
RT "Human interstitial retinoid-binding protein. Gene structure and
RL primary structure.";
RL J. Biol. Chem. 264:8200-8206(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90154038; PubMed=2303470;
RA Fong S.-L., Fong W.B., Morris T.A., Kedzie K.M., Bridges C.D.B.;
RT "Characterization and comparative structural features of the gene for
RL human interstitial retinol-binding protein.";
RL J. Biol. Chem. 265:3648-3653(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=9006790; PubMed=2792773;
RA Si J.S., Boirst D.E., Redmond T.M., Nickerson J.M.;

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RT "Cloning of cDNAs encoding human interphotoreceptor retinoid-binding
 RT protein (IRBP) and comparison with bovine IRBP sequences.";
 RL Gene 80:99-108(1989).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-88321820; PubMed-3455009;
 RA Liou G.I., Fong S.-L., Gosden J., van Tuinen P., Ledbetter D.H.,
 RA Christie S., Rout D., Bhattacharya S., Cook R.G., Li Y., Wang C.,
 RA Bridges C.D.B.;
 RT "Human interstitial retinol-binding protein (IRBP): cloning, partial
 RT sequence, and chromosomal localization.";
 RL Somat. Cell Mol. Genet. 13:315-323(1987).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89008429; PubMed-3170584;
 RA Fong S.-L., Bridges C.D.B.;
 RT "Internal quadruplication in the structure of human interstitial
 RT retinol-binding protein deduced from its cloned cDNA.";
 RL J. Biol. Chem. 265:15330-15334(1988).
 RN [6]
 RP SEQUENCE OF 1-382 FROM N.A.
 RX MEDLINE-90384818; PubMed-2402443;
 RA Albini A., Toffenetti J., Zhen Z., Chader G.J., Noonan D.M.;
 RT "Hypomethylation of the interphotoreceptor retinoid-binding protein
 RT (IRBP) promoter and first exon is linked to expression of the gene.";
 RL Nucleic Acids Res. 18:5181-5187(1990).
 RN [7]
 RP SEQUENCE OF 18-42.
 RX MEDLINE-87156570; PubMed-3827838;
 RA Redmond T.M., Wiggert B., Robey F.A., Chader G.J.;
 RT "Interspecies conservation of structure of interphotoreceptor
 RT retinoid-binding protein. Similarities and differences as adjudged
 RT by peptide mapping and N-terminal sequencing.";
 RL Biochem. J. 240:19-26(1986).
 RN [8]
 RP SEQUENCE OF 23-39.
 RX MEDLINE-86301171; PubMed-3743780;
 RA Fong S.-L., Cook R.G., Alvarez R.A., Liou G.I., Landers R.A.,
 RA Bridges C.D.B.;
 RT "N-terminal sequence homologies in interstitial retinol-binding
 RT proteins from 10 vertebrate species.";
 RL FEBS Lett. 205:309-312(1986).
 CC -1- FUNCTION: IRBP SHUTTLES 11-CIS AND ALL TRANS RETINOIDS BETWEEN
 CC THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL
 CC PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
 CC -1- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES
 CC THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT
 CC EPITHELIUM CELLS.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-2 IS THE INITIATOR.
 CC -1- CAUTION: REF. 4 AND REF. 5 SEQUENCES HAVE BEEN SHOWN TO BE INCORRECT
 CC AND THE REVISED SEQUENCE IS GIVEN IN REF.1, REF.2 AND REF.3.
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 CC -----
 CC DR EMBL: M33875; AAA59453.1; -;
 CC DR EMBL: M33864; AAA59453.1; JOINED.
 CC DR EMBL: M33865; AAA59453.1; JOINED.
 CC DR EMBL: M33866; AAA59453.1; JOINED.
 CC DR EMBL: M22453; AAA36126.1; -;
 CC DR EMBL: J05253; AAC18875.1; ALT_INIT.
 CC DR EMBL: J03912; AAA59188.1; -;
 CC DR EMBL: X53044; CAA37213.1; -;
 CC DR PIR: H24417; H24417.
 CC DR PIR: C25735; C25735.
 CC DR PIR: A31987; A31987.
 CC DR PIR: J50307; J50307.
 CC DR PIR: A33812; A33812.

DR Genew: HGNC:9921; RBP3.
 DR MIM: 180290; -;
 DR InterPro: IPR003581; TSPC.
 DR Pfam: PF02692; IRBP; 4.
 DR SMART: SM00245; TSPC; 4.
 KW Vitamin A; Transport; Repeat; Signal; Glycoprotein.
 FT SIGNAL 1 17
 FT CHAIN 18 1247
 FT
 FT DOMAIN 18 1230
 FT REPEAT 18 320
 FT REPEAT 321 630
 FT REPEAT 631 931
 FT REPEAT 932 1230
 FT CARBOHYD 205 205
 FT CARBOHYD 515 515
 SQ SEQUENCE 1247 AA; 135362 MW; 6C1841411E012E0F CRC64;
 Query Match 31.6%; Score 6; DB 1; Length 1247;
 Best local Similarity 100.0%; Pred. No. 42;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GGPTSS 16
 Db 1086 GGPTSS 1091

Search completed: January 7, 2003, 12:38:52
 Job time : 8.82051 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:37:03 : Search time 12.6667 Seconds
(without alignments)
144.202 Million cell updates/sec

Title: US-09-876-204-1

Perfect score: 19

Sequence: 1 MDGSGXXXXXGCPSSSEQI 19

Scoring table:

GAPOP 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

1: pir_73:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	47.4	143	2 I38921	bcl-2-associated p
2	9	47.4	179	2 JC7255	Bax-delta protein
3	9	47.4	192	2 A47538	bcl-2-associated p
4	9	47.4	192	2 D47538	bcl-2-associated p
5	9	47.4	218	2 B47538	bcl-2-associated p
6	6	31.6	105	2 PW0018	hypothetical prote
7	6	31.6	297	2 S33927	interphotoreceptor
8	6	31.6	298	2 S27965	interphotoreceptor
9	6	31.6	304	2 A49185	interphotoreceptor
10	6	31.6	337	2 I47079	follicularin - shee
11	6	31.6	344	1 A27701	follicularin precu
12	6	31.6	344	2 I45894	follicularin - bovi
13	6	31.6	364	2 I45915	interstitial retin
14	6	31.6	411	2 E96665	protein F22C12.16
15	6	31.6	441	2 S14441	retinol-binding pr
16	6	31.6	447	2 T19078	hypothetical prote
17	6	31.6	680	2 S37955	protein kinase ypk
18	6	31.6	790	2 S71278	DNA ligase (ATP) (
19	6	31.6	1028	2 I58164	BiG-1 protein - ra
20	6	31.6	1028	2 A53449	plasmacytoma-assoc
21	6	31.6	1147	2 T18770	probable calcium c
22	6	31.6	1247	2 A33812	interphotoreceptor
23	6	31.6	1286	1 RUBOP	interphotoreceptor
24	6	31.6	1576	2 S65774	homeotic protein H
25	6	31.6	2165	1 RNWZ2	genome polyprotein
26	6	31.6	2245	2 T18278	myosin heavy chain
27	6	26.3	41	2 C47538	bcl-2-associated p
28	5	26.3	53	2 H82571	hypothetical prote
29	5	26.3	69	2 C83855	hypothetical prote

30	5	26.3	72	2 T26662	hypothetical prote
31	5	26.3	74	2 C42266	peptidylglycine mo
32	5	26.3	74	2 T26665	hypothetical prote
33	5	26.3	82	2 D72280	conserved hypothet
34	5	26.3	84	2 S33328	hirudin HMI - leec
35	5	26.3	98	2 S48605	hypothetical prote
36	5	26.3	103	2 D71224	hypothetical prote
37	5	26.3	109	2 S51134	genome polyprotein
38	5	26.3	115	2 B49094	methylmalonyl-CoA
39	5	26.3	120	2 AG0808	conserved hypothet
40	5	26.3	120	2 JC2475	growth hormone reg
41	5	26.3	140	2 AH1917	hypothetical prote
42	5	26.3	142	2 T47212	ccg-8 protein limp
43	5	26.3	151	2 C84514	hypothetical prote
44	5	26.3	153	2 B72721	hypothetical prote
45	5	26.3	163	2 T22481	hypothetical prote

ALIGNMENTS

RESULT 1
I38921
bcl-2-associated protein x, delta splice form - human
N:Alternate names: BAX; programmed cell death membrane protein x delta
C:Species: Homo sapiens (man)
C:Date: 09-Mar-1996 #sequence,revision 09-Mar-1996 #text,change 17-Nov-2000
C:Accession: I38921
R:Appt, S.S.; Mattei, M.G.; Olsen, B.R.
Genomics 26, 592-594, 1995
A>Title: Mapping of the human BAX gene to chromosome 19q13.3-q13.4 and isolation of a
A:Reference number: I38921; MID:95331797; PMID:7607685
A:Accession: I38921
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-143 <RES>
A:Cross-references: EMBL:U01959; NID:g841237; PIDN:AMC50142.1; PID:g841238
C:Genetics:
A:Gene: GDB:BAX
A:Cross-references: GDB:228082; OMIM:600040
A:Map position: 19q13.3-19q13.4
C:Superfamily: bcl transforming protein

Query Match
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSSEQI 19
DB 11 GGPTSSSEQI 19

RESULT 2
JC7255
Bax-delta protein - human
C:Species: Homo sapiens (man)
C:Date: 09-Jun-2000 #sequence,revision 09-Jun-2000 #text,change 17-Nov-2000
C:Accession: JC7255
R:Schmitt, E.; Paquet, C.; Beauchemin, M.; Dever-Bertrand, J.; Bertrand, R.
Biochem. Biophys. Res. Commun. 270, 868-879, 2000
A>Title: Characterization of Bax-delta, a cell death-inducing isoform of Bax.
A:Reference number: JC7255
A:Accession: JC7255
A:Molecule type: mRNA
A:Residues: 1-179 <SCH>
A:Cross-references: GB:AF247393
A:Experimental source: cancer promyelocytic cells
C:Comment: This protein, a member of the Bcl-2 family, has a proapoptotic effect. It
C:Superfamily: bcl transforming protein
C:Keywords: transmembrane protein

Query Match
47.4%; Score 9; DB 2; Length 179;

Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GGPTSSQEI 19
Db 11 GGPTSSQEI 19

RESULT 3

A47538
bcl-2-associated protein x, alpha splice form - human
N:Alternate names: BAX; programmed cell death membrane protein x alpha
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C:Accession: A47538
R:Oltvai, Z.N.; Millman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates
A:Reference number: A47538; MUID:93364978; PMID:8358790
A:Accession: A47538
A:Molecule type: mRNA
A:Residues: 1-192 <OUT>
A:Cross-references: GB:L22473; NID:g388165; PIDN:AAA03619.1; PID:g388166
A:Note: the amino end of the mature protein is blocked
C:Genetics:
A:Gene: GDB:BAX
A:Cross-references: GDB:228082; OMIM:600040
A:Map position: 19q13.3-19q13.4
C:Superfamily: bcl transforming protein
C:Keywords: alternative splicing; blocked amino end; heterodimer; homodimer; transmembr
F:172-191/Domain: transmembrane status predicted <TM1>

Query Match 47.4%; Score 9; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSQEI 19
Db 11 GGPTSSQEI 19

RESULT 4

D47538
bcl-2-associated protein x - mouse
N:Alternate names: BAX; programmed cell death membrane protein x
C:Species: Mus musculus (house mouse)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C:Accession: D47538
R:Oltvai, Z.N.; Millman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates
A:Reference number: A47538; MUID:93364978; PMID:8358790
A:Accession: D47538
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-192 <OUT>
A:Cross-references: GB:L22472
C:Genetics:
A:Gene: bax
C:Superfamily: bcl transforming protein

Query Match 47.4%; Score 9; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSQEI 19
Db 11 GGPTSSQEI 19

RESULT 5

B47538
bcl-2-associated protein x, beta splice form - human

N:Alternate names: BAX; programmed cell death membrane protein x beta
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C:Accession: B47538
R:Oltvai, Z.N.; Millman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerate

A:Reference number: A47538; MUID:93364978; PMID:8358790
A:Accession: B47538
A:Molecule type: mRNA
A:Residues: 1-218 <OUT>

A:Cross-references: GB:L22474; NID:g388167; PIDN:AAA03620.1; PID:g388168
A:Note: the amino end of the mature protein is blocked
C:Genetics:
A:Gene: GDB:BAX

A:Cross-references: GDB:228082; OMIM:600040
A:Map position: 19q13.3-19q13.4
C:Superfamily: bcl transforming protein
C:Keywords: alternative splicing; blocked amino end; cytosol; heterodimer; homodimer

Query Match 47.4%; Score 9; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.0082;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSQEI 19
Db 11 GGPTSSQEI 19

RESULT 6

PW0018
hypothetical protein 105 - Micromonospora sp. (fragment)
C:Species: Micromonospora sp.
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Oct-1994
C:Accession: PW0018
R:Kelman, G.H.; Cundliffe, E.; Financsek, I.
Gene 98, 53-60, 1991
A:Title: Cloning and characterization of gentamicin-resistance genes from Micromonosp
A:Reference number: JG0017; MUID:91192615; PMID:2013410
A:Accession: PW0018
A:Molecule type: DNA
A:Residues: 1-105 <KFL>
A:Cross-references: GB:M55521
A:Note: the authors translated the codon CCG for residues 27, 30, 31, and 37 as Phe a

Query Match 31.6%; Score 6; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSS 16
Db 81 GGPTSS 86

RESULT 7

S33927
interphotoreceptor retinoid-binding protein - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C:Accession: S33927
R:Gonzalez-Fernandez, F.; Kittredge, K.L.; Rayborn, M.E.; Hollyfield, J.G.; Landers,
J. Cell Sci. 105, 7-21, 1993
A:Title: Interphotoreceptor retinoid-binding protein (IRBP), a major 124 kDa glycopro
A:Reference number: S33927; MUID:93366942; PMID:8360278
A:Accession: S33927
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-297 <GON>
A:Cross-references: EMBL:X69469; NID:g313172; PIDN:CAA49228.1; PID:g313173
C:Superfamily: interphotoreceptor retinoid-binding protein
C:Keywords: duplication

Query Match 31.6%; Score 6; DB 2; Length 297;

Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GGPTSS 16
|||||
Db 145 GGPTSS 150
RESULT 8
S27965
hypothetical protein - human
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 08-Sep-2000
C:Accession: S27965
R:Pollard, K.M.
submitted to the EMBL Data Library, June 1991
A:Reference number: S27965
A:Accession: S27965
A:Molecule type: mRNA
A:Residues: 1-298 <POL>
A:Cross-references: EMBL:M68864; NID:q189396; PION:AAA36396.1; PID:q189397
C:Superfamily: Caenorhabditis elegans hypothetical protein F23C8.4
Query Match 31.6%; Score 6; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 PRSSEQ 18
|||||
Db 64 PRSSEQ 69
RESULT 9
A49185
interphotoreceptor retinoid-binding protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Nov-1997
C:Accession: A49185
R:Gonzalez-Fernandez, F.; Van Niel, E.; Edmonds, C.; Beaver, H.; Nickerson, J.M.; Garcia
Exp. Eye Res. 36, 411-427, 1993
A:Title: Differential expression of interphotoreceptor retinoid-binding protein, opsin,
A:Reference number: A49185; MUID:93272869; PMID:7916695
A:Accession: A49185
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-304 <GON>
A:Note: sequence extracted from NCBI backbone (NCBIN:133270, NCBI:133271)
C:Superfamily: interphotoreceptor retinoid-binding protein
C:Keywords: duplication
Query Match 31.6%; Score 6; DB 2; Length 304;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GGPTSS 16
|||||
Db 154 GGPTSS 159
RESULT 10
147079
folliclstatin - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 20-Apr-2001
C:Accession: 147079
R:Tisdall, D.J.; Hill, D.; Petersen, G.B.; Fleming, J.S.
J. Mol. Endocrinol. 8, 259-264, 1992
A:Title: Ovine folliclstatin: characterization of cDNA and expression in sheep ovary durin
A:Reference number: 147079; MUID:92337809; PMID:1632897
A:Accession: 147079
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-337 <TIS>

A:Cross-references: GB:M63123; NID:q165882; PIDN:AAA31522.1; PID:q165883
C:Superfamily: folliclstatin; Kazal proteinase inhibitor homology
F:107-157/Domain: Kazal proteinase inhibitor homology <KPI1>
F:181-232/Domain: Kazal proteinase inhibitor homology <KPI2>
F:258-309/Domain: Kazal proteinase inhibitor homology <KPI3>
Query Match 31.6%; Score 6; DB 2; Length 337;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 PRSSEQ 18
|||||
Db 192 PRSSEQ 197
RESULT 11
A27701
folliclstatin precursor - pig
N:Contains: folliclstatin short form precursor
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 17-Nov-2000
C:Accession: A27701; A40064; B40064; A39969; A47139
R:Shimasaki, S.; Koga, M.; Esch, F.; Mercado, M.; Cooksey, K.; Koba, A.; Ling, N.
Biochem. Biophys. Res. Commun. 152, 717-723, 1988
A:Title: Porcine folliclstatin gene structure supports two forms of mature folliclstatin
A:Reference number: A27701; MUID:88209050; PMID:3365249
A:Accession: A27701
A:Molecule type: DNA
A:Residues: 1-344 <SH1>
A:Cross-references: GB:M19529; NID:q164458; PIDN:AAA31036.1; PID:q164459
R:Esch, F.S.; Shimasaki, S.; Mercado, M.; Cooksey, K.; Ling, N.; Yeno, N.;
Mol. Endocrinol. 1, 849-855, 1987
A:Title: Structural characterization of folliclstatin: a novel follicle-stimulating hor
A:Reference number: A40064; MUID:91042571; PMID:3153465
A:Accession: A40064
A:Molecule type: mRNA
A:Residues: 1-344 <ESC1>
A:Cross-references: GB:M36512; GB:M36513; NID:q164461
A:Accession: B40064
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-317 <ESC2>
A:Cross-references: GB:M36512; GB:M36513; NID:q164461
R:Yeno, N.; Ling, N.; Ying, S.Y.; Esch, F.; Shimasaki, S.; Guillemin, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 8282-8286, 1987
A:Title: Isolation and partial characterization of folliclstatin: a single-chain M-r 35
A:Reference number: A39969; MUID:88068578; PMID:3120188
A:Accession: A39969
A:Molecule type: protein
A:Residues: 30-37 <UEN>
R:Sugino, K.; Kurosawa, N.; Nakamura, T.; Takio, K.; Shimasaki, S.; Ling, N.; Titani,
J. Biol. Chem. 268, 15579-15587, 1993
A:Title: Molecular heterogeneity of folliclstatin, an activin-binding protein. Higher a
A:Reference number: A47139; MUID:93340158; PMID:8340284
A:Accession: A47139
A:Status: preliminary
A:Molecule type: protein
A:Residues: 30-35;120-128;284-292;312-344 <SUG>
C:Comment: Folliclstatin inhibits release of pituitary follicle stimulating hormone.
C:Genetics:
A:introns: 29/1; 93/1; 166/1; 241/1; 318/1
C:Superfamily: folliclstatin; Kazal proteinase inhibitor homology
C:Keywords: alternative splicing; glycoprotein; monomer
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-344/Product: folliclstatin #status predicted <MAS>
F:30-317/Product: folliclstatin, short splice form #status predicted <MAS>
F:114-164/Domain: Kazal proteinase inhibitor homology <KPI8>
Query Match 31.6%; Score 6; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 PRSSEQ 18

Db 199 PTSSEQ 204

RESULT 12

145894
foliistatin - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 17-Nov-2000
C:Accession: 145894
R: Houde, A.; Lussier, J.G.; Ethier, J.F.; Gagnon, C.; Silversides, D.W.
Mol. Reprod. Dev. 37, 391-397, 1994
A:Title: Cloning and tissue expression of bovine foliistatin cDNA.
A:Reference number: 145894; MUID:94280841; PMID:8011323
A:Accession: 145894
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-344 <HOU>
A:Cross-references: GB:L21716; NID:g404023; PIDN:AAA30522.1; PID:g404024
C:Superfamily: foliistatin; Kazal proteinase inhibitor homology
F:114-164/Domain: Kazal proteinase inhibitor homology <KPI1>
F:187-239/Domain: Kazal proteinase inhibitor homology <KPI2>
F:265-316/Domain: Kazal proteinase inhibitor homology <KPI3>

Query Match 31.6%; Score 6; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 PTSSEQ 18
Db 199 PTSSEQ 204

RESULT 13

145915
interstitial retinol binding protein - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 13-Aug-1999
C:Accession: 145915
R: Liou, G.I.; Fong, S.
Vision Res. 26, 1645-1653, 1986
A:Title: Bovine interstitial retinol-binding protein (IRBP)-isolation and sequence analysis.
A:Reference number: 145915; MUID:87293907; PMID:3617506
A:Accession: 145915
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-364 <LIO>
A:Cross-references: GB:M19390; NID:g163232; PIDN:AAA30592.1; PID:g163235
C:Superfamily: interphotoreceptor retinoid-binding protein
C:Keywords: duplication

Query Match 31.6%; Score 6; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GGPTSS 16
Db 162 GGPTSS 167

RESULT 14

E96665
protein F22C12.16 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: E96665
R: Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E96665
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-411 <STO>
A:Cross-references: GB:AE005173; NID:g6692100; PIDN:AAF24565.1; GSPDB:GN00141
C:Genetics:
A:Gene: F22C12.16
A:Map position: 1

Query Match 31.6%; Score 6; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 PTSSEQ 18
Db 134 PTSSEQ 139

RESULT 15

S14441
retinol-binding protein, interstitial - bovine (fragments)
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 31-Oct-1997
C:Accession: S14441
R: Liou, G.I.; Fong, S.L.; Gosden, J.; Van Thunen, P.; Leebetter, D.H.; Christie, S.; Somat, Cell Mol. Genet. 13, 315-323, 1987
A:Title: Human interstitial retinol-binding protein (IRBP): cloning, partial sequence analysis.
A:Reference number: S06277; MUID:88321820; PMID:3455009
A:Accession: S14441
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-31; 32-38; 39-72; 73-129; 130-143; 144-171; 172-199; 200-213; 214-441 <BOV>
C:Superfamily: interphotoreceptor retinoid-binding protein
C:Keywords: duplication; glycoprotein

Query Match 31.6%; Score 6; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GGPTSS 16
Db 286 GGPTSS 291

Search completed: January 7, 2003, 12:40:22
Job time: 14.6667 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:38:59 : Search time 11.2051 Seconds
(without alignments)
120.181 Million cell updates/sec

Title: US-09-876-204-1
Perfect score: 19
Sequence: 1 MDGSGXXXXGGPTSSQI 19

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 262191 seqs, 70875818 residues

Word size: 0

Total number of hits satisfying chosen parameters: 262191

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCt_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
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7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	47.4	191	6	US-10-196-793A-46
2	9	47.4	192	1	PCT-US02-38191-5
3	9	47.4	192	6	US-10-306-878-5
4	6	31.6	94	1	PCT-US02-32727-10714
5	6	31.6	94	6	US-10-057-498-10714
6	6	31.6	120	6	US-10-092-411A-5332
7	6	31.6	586	6	US-10-258-951-54
8	6	31.6	748	5	US-09-134-000C-6041
9	6	31.6	4219	6	US-10-085-198-2
10	5	26.3	15	6	US-10-308-128-65
11	5	26.3	21	7	US-60-427-045-298
12	5	26.3	49	6	US-10-203-138A-13021
13	5	26.3	49	6	US-10-218-102-365
14	5	26.3	50	1	PCT-US02-32727-19622
15	5	26.3	50	6	US-10-057-498-19622
16	5	26.3	52	1	PCT-US02-32727-18710
17	5	26.3	52	6	US-10-057-498-18710
18	5	26.3	53	6	US-10-276-781-1619
19	5	26.3	54	1	PCT-US02-32727-6231
20	5	26.3	54	6	US-10-057-498-6231
21	5	26.3	58	1	PCT-US02-32727-16184
22	5	26.3	58	6	US-10-057-498-16184
23	5	26.3	60	1	PCT-US02-32727-12723
24	5	26.3	60	1	US-09-513-999C-7514
25	5	26.3	60	6	US-10-057-498-12723
26	5	26.3	62	1	PCT-US02-32727-2995

27	5	26.3	62	1	PCT-US02-32727-27998	Sequence 27998, A
28	5	26.3	62	6	US-10-057-498-2995	Sequence 2995, Ap
29	5	26.3	62	6	US-10-057-498-27998	Sequence 27998, A
30	5	26.3	67	1	PCT-US02-32727-2249	Sequence 2249, Ap
31	5	26.3	67	6	US-10-057-498-2249	Sequence 2249, Ap
32	5	26.3	68	1	PCT-US02-32727-1219	Sequence 1219, Ap
33	5	26.3	68	6	US-09-134-000C-4348	Sequence 4348, Ap
34	5	26.3	68	6	US-10-057-498-1219	Sequence 1219, Ap
35	5	26.3	71	1	PCT-US02-32727-23986	Sequence 23986, A
36	5	26.3	71	6	US-10-057-498-23986	Sequence 23986, A
37	5	26.3	76	1	PCT-US02-32727-7217	Sequence 7217, Ap
38	5	26.3	76	6	US-10-057-498-7217	Sequence 7217, Ap
39	5	26.3	86	1	PCT-US02-32727-24556	Sequence 24556, A
40	5	26.3	88	6	US-10-057-498-24556	Sequence 24556, A
41	5	26.3	90	1	PCT-US02-32727-18175	Sequence 18175, A
42	5	26.3	90	6	US-10-057-498-18175	Sequence 18175, A
43	5	26.3	93	1	PCT-US02-32727-11127	Sequence 11127, A
44	5	26.3	93	6	US-10-057-498-11127	Sequence 11127, A
45	5	26.3	98	6	US-10-209-582-738	Sequence 738, App

ALIGNMENTS

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RESULT 1
US-10-196-793A-46
Sequence 46, Application US/10196793A
GENERAL INFORMATION:
APPLICANT: LIU, YUYING
TITLE OF INVENTION: THERAPEUTIC AGENTS COMPRISING PRO-APOPTOTIC PROTEINS
FILE REFERENCE: CLR:01205
CURRENT APPLICATION NUMBER: US/10/196,793A
CURRENT FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 60/360,361
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: 60/332,886
PRIOR FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: 60/306,091
PRIOR FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
LENGTH: 191
TYPE: PRT
ORGANISM: Homo sapiens
US-10-196-793A-46

Query Match
Best Local Similarity 47.4%; Score 9; DB 6; Length 191;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSQI 19
Db 10 GGPTSSQI 18

RESULT 2
PCT-US02-38191-5
Sequence 5, Application PC/TUS0238191
GENERAL INFORMATION:
APPLICANT: The Burnham Institute
APPLICANT: Reed, John C.
APPLICANT: Guo, Bin
TITLE OF INVENTION: Methods for Identifying Modulators of
FILE REFERENCE: FP-LJ 5483
CURRENT APPLICATION NUMBER: PCT/US02/38191
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: US 60/334,149
PRIOR FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSQ for Windows Version 4.0
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; SEQ ID NO 5
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-38191-5

Query Match 47.4%; Score 9; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GGPTSSSEOI 19
Db 11 GGPTSSSEOI 19

RESULT 3
US-10-306-878-5
; Sequence 5, Application US/10306878
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Guo, Bin
; TITLE OF INVENTION: Methods for Identifying Modulators of
; TITLE OF INVENTION: Apoptosis
; FILE REFERENCE: P-LJ 5535
; CURRENT APPLICATION NUMBER: US/10/306, 878
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US 60/334,149
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-306-878-5

Query Match 47.4%; Score 9; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GGPTSSSEOI 19
Db 11 GGPTSSSEOI 19

RESULT 4
PCT-US02-32727-10714
; Sequence 10714, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 10714
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Propionibacterium acnes
PCT-US02-32727-10714

Query Match 31.6%; Score 6; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 GPTSSSE 17
Db 30 GPTSSSE 35

RESULT 5
US-10-057-498-10714
; Sequence 10714, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 10714
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Propionibacterium acnes
US-10-057-498-10714

Query Match 31.6%; Score 6; DB 6; Length 94;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 GPTSSSE 17
Db 30 GPTSSSE 35

RESULT 6
US-10-092-411A-5332
; Sequence 5332, Application US/10092411A
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-101
; CURRENT APPLICATION NUMBER: US/10/092,411A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5676
; SEQ ID NO 5332
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-5332

Query Match 31.6%; Score 6; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 PTSSSEOI 18
Db 54 PTSSSEOI 59

RESULT 7
US-10-258-951-54
; Sequence 54, Application US/10258951
; GENERAL INFORMATION:

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; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kahnlick, Karen
; APPLICANT: Lai, Ying-Ta
; APPLICANT: Xie, Qing
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50025
; CURRENT APPLICATION NUMBER: US/10/258,951
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/13360
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/199,963
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/203,336
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/207,087
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/207,546
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-258-951-54
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Query Match          31.6%; Score 6; DB 6; Length 586;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 14 TSSEQ1 19
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Db 542 TSSEQ1 547
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RESULT 8
US-09-134-000C-6041
; Sequence 6041, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032/96-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6041
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6041
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Query Match          31.6%; Score 6; DB 5; Length 748;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 11 GGPTSS 16
      |||||
Db 41 GGPTSS 46
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RESULT 9
US-10-085-198-2
; Sequence 2, Application US/10085198
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
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; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-279
; CURRENT APPLICATION NUMBER: US/10/085,198
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-085-198-2
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Query Match          31.6%; Score 6; DB 6; Length 4219;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 11 GGPTSS 16
      |||||
Db 1549 GGPTSS 1554
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RESULT 10
US-10-308-128-65
; Sequence 65, Application US/10308128
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL HUMAN MITOCHONDRIAL AND MICROSO
; FILE REFERENCE: D0199 NP
; CURRENT APPLICATION NUMBER: US/10/308,128
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: U.S. 60/334,904
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-308-128-65
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Query Match          26.3%; Score 5; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 11 GGPTS 15
      |||||
Db 6 GGPTS 10
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RESULT 11
US-60-427-045-298
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Sequence 298, Application US/60427045
GENERAL INFORMATION:
APPLICANT: The Board of Trustees of the University of Arkansas
APPLICANT: O'Brien, Timothy
APPLICANT: Beard, John
APPLICANT: Underwood, Lowell
TITLE OF INVENTION: CA125 Gene and its use for Diagnostic and Therapeutic
FILE REFERENCE: 022438.44514
CURRENT APPLICATION NUMBER: US/60/427,045
CURRENT FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 314
SOFTWARE: PatentIn version 3.2
SEQ ID NO 298
LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens
US-60-427-045-298

Query Match 26.3%; Score 5; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PTSSE 17
Db 16 PTSSE 20

RESULT 12
US-10-203-138A-13021
Sequence 13021, Application US/10203138A
GENERAL INFORMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: PB 0004 WO 8
CURRENT APPLICATION NUMBER: US/10/203,138A
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 21 September 2000 (21.09.00)
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 30 June 2000 (30.06.00)
NUMBER OF SEQ ID NOS: 15438
SOFTWARE: Molecular Dynamics Sequence Listing Engine
SEQ ID NO 13021
LENGTH: 49
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL109942.4
FEATURE:
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.3
FEATURE:
OTHER INFORMATION: EST_HUMAN HIT: BE707262.1, EVALUATE 3.90e+00
US-10-203-138A-13021

Query Match 26.3%; Score 5; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GPTSS 16
Db 33 GPTSS 37

RESULT 13
US-10-218-102-365
Sequence 365, Application US/10218102
GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg
APPLICANT: Danylac, Basill I.
APPLICANT: Desjarlais, John R.
APPLICANT: Hayes, Robert J.
APPLICANT: Vielmetter, Jost
TITLE OF INVENTION: Protein Design Automation for Protein Libraries
FILE REFERENCE: A-67229-11/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/10/218,102
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: US 09/927,790
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/311,545
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US 60/324,899
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/351,937
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/352,103
NUMBER OF SEQ ID NOS: 432
SOFTWARE: PatentIn version 3.1
SEQ ID NO 365
LENGTH: 49
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
US-10-218-102-365

Query Match 26.3%; Score 5; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TSSQ 18
Db 11 TSSQ 15

RESULT 14
PCT-US02-32727-19622
Sequence 19622, Application PCT/TUS0232727
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
APPLICANT: Bhatia, Ajay
APPLICANT: Maisonneuve, Jean Francois
APPLICANT: Zhang, Yanni
APPLICANT: Wang, Siding
APPLICANT: Jen, Shyian
APPLICANT: Lodes, Michael
APPLICANT: Benson, Darin
APPLICANT: Jones, Robert
APPLICANT: Carter, Darlick
APPLICANT: Barth, Brenda
APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 19622
LENGTH: 50

; TYPE: PRT
; ORGANISM: Propioni|acnes
PCT-US02-32727-19622

Query Match 26.3%; Score 5; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GPTSS 16
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|
|
|
Db 35 GPTSS 39

RESULT 15
US-10-057-498-19622
; Sequence 19622, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 19622
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-19622

Query Match 26.3%; Score 5; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GPTSS 16
|
|
|
|
Db 35 GPTSS 39

Search completed: January 7, 2003, 12:46:01
Job time : 12.2051 secs

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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:38:34 : Search time 133 Seconds
(without alignments)
92.105 Million cell updates/sec

Title: US-09-876-204-1

Perfect score: 19

Sequence: 1 MDGSGXXXXXGPTSSBQI 19

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 4569144 seqs, 644733110 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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26: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	73.7	19	22	US-09-876-204-1
2	9	47.4	20	22	US-09-876-204-3
3	9	47.4	20	22	US-09-876-204-4
4	9	47.4	20	22	US-09-876-204-5
5	9	47.4	70	1	PCT-US99-24747-1
6	9	47.4	70	1	PCT-US99-24747-2

7	9	47.4	70	1	PCT-US99-24747-5	Sequence 5, Appli
8	9	47.4	70	1	PCT-US99-24747-6	Sequence 6, Appli
9	9	47.4	70	15	US-09-177-315-1	Sequence 1, Appli
10	9	47.4	70	15	US-09-177-315-2	Sequence 2, Appli
11	9	47.4	70	15	US-09-177-315-5	Sequence 5, Appli
12	9	47.4	70	15	US-09-177-315-6	Sequence 6, Appli
13	9	47.4	78	1	PCT-US99-24747-3	Sequence 3, Appli
14	9	47.4	78	1	PCT-US99-24747-4	Sequence 4, Appli
15	9	47.4	78	1	PCT-US99-24747-7	Sequence 7, Appli
16	9	47.4	78	1	PCT-US99-24747-8	Sequence 8, Appli
17	9	47.4	78	15	US-09-177-315-3	Sequence 3, Appli
18	9	47.4	78	15	US-09-177-315-4	Sequence 4, Appli
19	9	47.4	78	15	US-09-177-315-7	Sequence 7, Appli
20	9	47.4	78	15	US-09-177-315-8	Sequence 8, Appli
21	9	47.4	131	1	PCT-US99-05359-2	Sequence 2, Appli
22	9	47.4	131	16	US-09-266-465-2	Sequence 2, Appli
23	9	47.4	135	1	PCT-US02-06951-242	Sequence 242, App
24	9	47.4	135	24	US-10-092-750-242	Sequence 242, App
25	9	47.4	143	21	US-09-791-537-52874	Sequence 52874, A
26	9	47.4	143	27	US-60-350-061-261	Sequence 261, App
27	9	47.4	164	21	US-09-791-537-105329	Sequence 105329
28	9	47.4	192	1	PCT-US98-19765-45	Sequence 45, Appli
29	9	47.4	192	1	PCT-US98-19765-46	Sequence 46, Appli
30	9	47.4	192	1	PCT-US99-05359-4	Sequence 4, Appli
31	9	47.4	192	1	PCT-US99-24747-12	Sequence 12, Appli
32	9	47.4	192	1	PCT-US99-24747-13	Sequence 13, Appli
33	9	47.4	192	5	US-08-112-208B-5	Sequence 5, Appli
34	9	47.4	192	5	US-08-112-208B-6	Sequence 6, Appli
35	9	47.4	192	5	US-08-160-067-7	Sequence 7, Appli
36	9	47.4	192	6	US-08-248-819-5	Sequence 5, Appli
37	9	47.4	192	6	US-08-248-819-6	Sequence 6, Appli
38	9	47.4	192	7	US-08-320-157-13	Sequence 13, Appli
39	9	47.4	192	8	US-08-470-865-13	Sequence 13, Appli
40	9	47.4	192	8	US-08-483-233-2	Sequence 2, Appli
41	9	47.4	192	8	US-08-483-233-3	Sequence 3, Appli
42	9	47.4	192	8	US-08-483-233-8	Sequence 8, Appli
43	9	47.4	192	8	US-08-483-233-9	Sequence 9, Appli
44	9	47.4	192	8	US-08-483-233A-2	Sequence 2, Appli
45	9	47.4	192	8	US-08-483-233A-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-876-204-1
; Sequence 1, Application US/09876204
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; REAGENTS AND METHODS
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/876, 204
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/166, 028
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic based on consensus sequence of Homo
; sapiens, Mus musculus, and Rattus norvegicus
; NAME/KEY: VARIANT
; LOCATION: (6)...(10)
; OTHER INFORMATION: Xaa at 6 can be E or D; Xaa at 7 can be Q or H;
; OTHER INFORMATION: Xaa at 8 can be L or P; Xaa at 9 can be R or G;
; OTHER INFORMATION: Xaa at 10 can be S or G;
US-09-876-204-1

Query Match 73.7% Score 14: DB 22; Length 19;

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Best Local Similarity 100.0%; Pred. No. 4e-07; 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 1 MDGSGXXXXXGGPTSSSEQI 19
Db 1 MDGSGXXXXXGGPTSSSEQI 19

RESULT 2
US-09-876-204-3
; Sequence 3, Application US/09876204
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/876,204
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/166,028
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-204-3

Query Match 47.4%; Score 9; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.056; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19

RESULT 3
US-09-876-204-4
; Sequence 4, Application US/09876204
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/876,204
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/166,028
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-876-204-4

Query Match 47.4%; Score 9; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.056; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19

RESULT 4
US-09-876-204-5
; Sequence 5, Application US/09876204
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/876,204
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/166,028
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-876-204-5

Query Match 47.4%; Score 9; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.056; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19

RESULT 5
PCT-US99-24747-1
; Sequence 1, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-24747-1

Query Match 47.4%; Score 9; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.17; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19

RESULT 6
PCT-US99-24747-2
; Sequence 2, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US99-24747-2

Query Match 47.4%; Score 9; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.17; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19
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Db 11 GGPTSSEQI 19

RESULT 7
PCT-US99-24747-5
; Sequence 5, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-24747-5

Query Match 47.4%; Score 9; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
|||||
Db 11 GGPTSSEQI 19

RESULT 8
PCT-US99-24747-6
; Sequence 6, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US99-24747-6

Query Match 47.4%; Score 9; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
|||||
Db 11 GGPTSSEQI 19

RESULT 9
US-09-177-315-1
; Sequence 1, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-5756
; CURRENT APPLICATION NUMBER: US/09/177,315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens

Query Match 47.4%; Score 9; DB 15; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
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Db 11 GGPTSSEQI 19

RESULT 10
US-09-177-315-2
; Sequence 2, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachel M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-5756
; CURRENT APPLICATION NUMBER: US/09/177,315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-177-315-2

Query Match 47.4%; Score 9; DB 15; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
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Db 11 GGPTSSEQI 19

RESULT 11
US-09-177-315-5
; Sequence 5, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-5756
; CURRENT APPLICATION NUMBER: US/09/177,315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-177-315-5

Query Match 47.4%; Score 9; DB 15; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
|||||
Db 11 GGPTSSEQI 19

RESULT 12
US-09-177-315-6
; Sequence 6, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachel M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-5756
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; CURRENT APPLICATION NUMBER: US/09/177,315
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-177-315-6

Query Match 47.4%; Score 9; DB 15; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19

RESULT 13
PCT-US99-24747-3
; Sequence 3, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-24747-3

Query Match 47.4%; Score 9; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19

RESULT 14
PCT-US99-24747-4
; Sequence 4, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US99-24747-4

Query Match 47.4%; Score 9; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19

RESULT 15
PCT-US99-24747-7
; Sequence 7, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-24747-7

Query Match 47.4%; Score 9; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19

Search completed: January 7, 2003, 12:45:31
Job time : 134 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:39:54 ; Search time 7.30769 Seconds
(without alignments)
49.274 Million cell updates/sec

Title: US-09-876-204-1

Perfect score: 19

Sequence: 1 MDGSGXXXXXGGPTSSSEQI 19

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- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US05_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	73.7	19	10	US-09-876-204-1
2	9	47.4	20	10	US-09-876-204-3
3	9	47.4	20	10	US-09-876-204-4
4	9	47.4	20	10	US-09-876-204-5
5	9	47.4	331	10	US-09-033-525-2
6	6	31.6	154	10	US-09-876-889-16
7	5	26.3	20	10	US-09-205-658-281
8	5	26.3	37	10	US-09-205-658-257
9	5	26.3	38	10	US-09-864-761-41953
10	5	26.3	49	10	US-09-864-761-35963
11	5	26.3	50	10	US-09-864-761-38835
12	5	26.3	77	9	US-10-001-835-143
13	5	26.3	89	10	US-09-764-869-948
14	5	26.3	116	10	US-09-764-853-501
15	5	26.3	243	9	US-09-738-626-5718
16	5	26.3	253	10	US-09-764-870-424
17	5	26.3	258	9	US-09-738-626-4896
18	5	26.3	275	10	US-09-054-141-2
19	5	26.3	324	10	US-09-886-055-81

20	5	26.3	438	10	US-09-884-441-390	Sequence 390, Appl
21	5	26.3	438	10	US-09-884-441-483	Sequence 483, Appl
22	5	26.3	440	9	US-10-063-547-134	Sequence 134, Appl
23	5	26.3	440	12	US-10-006-867-134	Sequence 134, Appl
24	5	26.3	440	12	US-10-052-586-386	Sequence 386, Appl
25	5	26.3	450	9	US-09-866-570A-67	Sequence 67, Appl
26	5	26.3	450	10	US-09-866-572A-67	Sequence 67, Appl
27	5	26.3	451	9	US-09-902-772-2	Sequence 2, Appl
28	5	26.3	478	9	US-09-902-772-4	Sequence 4, Appl
29	5	26.3	494	12	US-10-143-002-4	Sequence 4, Appl
30	5	26.3	503	10	US-09-925-297-577	Sequence 577, Appl
31	5	26.3	509	10	US-09-864-761-35112	Sequence 35112, A
32	5	26.3	527	9	US-09-738-626-4962	Sequence 4962, Ap
33	5	26.3	533	10	US-09-908-805B-63	Sequence 63, Appl
34	5	26.3	568	9	US-09-738-626-5622	Sequence 5622, Ap
35	5	26.3	568	10	US-09-950-788-2	Sequence 2, Appl
36	5	26.3	568	10	US-09-950-788-4	Sequence 4, Appl
37	5	26.3	568	10	US-09-950-788-7	Sequence 7, Appl
38	5	26.3	579	9	US-09-922-364A-19	Sequence 19, Appl
39	5	26.3	579	9	US-09-254-590-19	Sequence 19, Appl
40	5	26.3	579	9	US-10-115-695-19	Sequence 19, Appl
41	5	26.3	580	9	US-09-922-364A-2	Sequence 2, Appl
42	5	26.3	580	9	US-09-254-590-2	Sequence 2, Appl
43	5	26.3	580	9	US-10-115-695-2	Sequence 2, Appl
44	5	26.3	597	10	US-09-815-242-13226	Sequence 13226, A
45	5	26.3	645	10	US-09-925-300-1453	Sequence 1453, Ap

ALIGNMENTS

RESULT 1
US-09-876-204-1
; Sequence 1, Application US/09876204
; Patent No. US20020052316A1
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; REAGENTS AND METHODS
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/876, 204
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/166,028
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic based on consensus sequence of Homo
; sapiens, Mus musculus, and Rattus norvegicus
; NAME/KEY: VARIANT
; LOCATION: (6)...(10)
; OTHER INFORMATION: Xaa at 6 can be E or D; Xaa at 7 can be Q or H;
; OTHER INFORMATION: Xaa at 8 can be L or P; Xaa at 9 can be R or G;
; OTHER INFORMATION: Xaa at 10 can be S or G;
US-09-876-204-1

Query Match 73.7% Score 14; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDGSGXXXXXGGPTSSSEQI 19
Db 1 MDGSGXXXXXGGPTSSSEQI 19

RESULT 2
US-09-876-204-3
; Sequence 3, Application US/09876204
; Patent No. US20020052316A1

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; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; FILE OF INVENTION: REAGENTS AND METHODS
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/876,204
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/166,028
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-204-3

Query Match          47.4%; Score 9; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19

RESULT 3
US-09-876-204-4
; Sequence 4, Application US/09876204
; Patent No. US20020052316A1
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; FILE OF INVENTION: REAGENTS AND METHODS
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/876,204
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/166,028
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-876-204-4

Query Match          47.4%; Score 9; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19

RESULT 4
US-09-876-204-5
; Sequence 5, Application US/09876204
; Patent No. US20020052316A1
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; FILE OF INVENTION: REAGENTS AND METHODS
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/876,204
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/166,028
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-876-204-5
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; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-876-204-5

Query Match          47.4%; Score 9; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19

RESULT 5
US-09-033-525-2
; Sequence 2, Application US/09033525
; Patent No. US20020090374A1
; GENERAL INFORMATION:
; APPLICANT: Yarkoni, Shai
; APPLICANT: Ben-Yehudah, Ahmi
; APPLICANT: Azar, Yehudith
; APPLICANT: Agellian, Rami
; APPLICANT: Belototsky, Ruth
; APPLICANT: Lorberbom-Galski, Haya
; TITLE OF INVENTION: CHIMERIC PROTEINS WITH CELL-TARGETING
; TITLE OF INVENTION: SPECIFICITY AND APOPTOSIS-INDUCING ACTIVITIES
; FILE REFERENCE: 9457-009-999
; CURRENT APPLICATION NUMBER: US/09/033,525
; CURRENT FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-033-525-2

Query Match          47.4%; Score 9; DB 10; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
Db 150 GGPTSSEQI 158

RESULT 6
US-09-876-889-16
; Sequence 16, Application US/09876889
; Patent No. US20020076715A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
; TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.466C3
; CURRENT APPLICATION NUMBER: US/09/876,889
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-876-889-16

Query Match          31.6%; Score 6; DB 10; Length 154;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PTSSEQ 18
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Db 64 PTSSEQ 69

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RESULT 7

US-09-205-658-281
; Sequence 281, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US98/10080
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 281
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-205-658-281

Query Match 26.3%; Score 5; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GPTSS 16

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Db 3 GPTSS 7

RESULT 8

US-09-205-658-257
; Sequence 257, Application US/09205658
; Patent No. US20010029617A1
; GENERAL INFORMATION:
; APPLICANT: Ruvkun, Gary
; APPLICANT: Ogg, Scott
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
; FILE REFERENCE: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
; CURRENT APPLICATION NUMBER: US/09/205,658
; CURRENT FILING DATE: 1998-12-03
; EARLIER FILING DATE: 1997-05-15
; EARLIER APPLICATION NUMBER: 08/857,076
; EARLIER FILING DATE: 1997-07-07
; EARLIER APPLICATION NUMBER: 08/888,534
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 328
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-205-658-257

Query Match 26.3%; Score 5; DB 10; Length 37;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTS 15

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Db 2 GGPTS 6

RESULT 9

US-09-864-761-41953
; Sequence 41953, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,587
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 41953
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC023344.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.8
US-09-864-761-41953

Query Match 26.3%; Score 5; DB 10; Length 38;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.7
; OTHER INFORMATION: SWISSPROT HIT: Q46378, EVALU6 4.70e+00
US-09-864-761-38835

Query Match 26.3%; Score 5; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTS 15
| | | | |
DB 42 GGPTS 46

RESULT 12
US-10-001-835-143
; Sequence 143, Application US/10001835
; Patent No. US20020160387A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Heirve
; APPLICANT: Cafferkey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro
; FILE REFERENCE: DEX-0277
; CURRENT APPLICATION NUMBER: US/10/001,835
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/249,997
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-835-143

Query Match 26.3%; Score 5; DB 9; Length 77;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GPTSS 16
| | | | |
DB 50 GPTSS 54

RESULT 13
US-09-764-869-948
; Sequence 948, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 948
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-869-948

Query Match 26.3%; Score 5; DB 10; Length 89;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PTSSE 17
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DB 44 PTSSE 48

RESULT 14
US-09-764-853-501
; Sequence 501, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ206
; CURRENT APPLICATION NUMBER: US/09/764,853
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 939
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 501
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-501

Query Match 26.3%; Score 5; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 PTSSE 17
| | | | |
DB 96 PTSSE 100

RESULT 15
US-09-738-626-5718
; Sequence 5718, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5718
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5718

Query Match 26.3%; Score 5; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 TSSEQ 18
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Tue Jan 7 13:10:43 2003

us-09-876-204-1.rapb

Page 6

Db 3 TSSEQ 7

Search completed: January 7, 2003, 12:46:23
Job time : 8.30769 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:37:29 ; Search time 11.2051 Seconds
(without alignments)
49.891 Million cell updates/sec

Title: USF-09-876-204-1

Perfect score: 19
Sequence: 1 MDGSGXXXXXGGPTSSEQI 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	73.7	19	US-09-166-028-1	Sequence 1, Appli
2	9	47.4	20	US-09-166-028-3	Sequence 3, Appli
3	9	47.4	20	US-09-166-028-4	Sequence 4, Appli
4	9	47.4	20	US-09-166-028-5	Sequence 5, Appli
5	9	47.4	25	US-08-798-897-21	Sequence 21, Appli
6	9	47.4	25	US-08-978-523-21	Sequence 21, Appli
7	9	47.4	192	US-08-112-208C-2	Sequence 2, Appli
8	9	47.4	192	US-08-112-208C-3	Sequence 3, Appli
9	9	47.4	192	US-08-112-208C-8	Sequence 8, Appli
10	9	47.4	192	US-08-112-208C-9	Sequence 9, Appli
11	9	47.4	192	US-08-248-819A-2	Sequence 2, Appli
12	9	47.4	192	US-08-248-819A-3	Sequence 3, Appli
13	9	47.4	192	US-08-248-819A-8	Sequence 8, Appli
14	9	47.4	192	US-08-248-819A-9	Sequence 9, Appli
15	9	47.4	192	US-08-607-269-25	Sequence 25, Appli
16	9	47.4	192	US-08-471-058-13	Sequence 13, Appli
17	9	47.4	192	US-08-337-646A-2	Sequence 2, Appli
18	9	47.4	192	US-08-337-646A-3	Sequence 3, Appli
19	9	47.4	192	US-08-337-646A-8	Sequence 8, Appli
20	9	47.4	192	US-08-337-646A-9	Sequence 9, Appli
21	9	47.4	192	US-08-856-531-2	Sequence 2, Appli
22	9	47.4	192	US-08-856-531-3	Sequence 3, Appli
23	9	47.4	192	US-08-856-531-8	Sequence 8, Appli
24	9	47.4	192	US-08-856-531-9	Sequence 9, Appli
25	9	47.4	192	US-08-856-034-2	Sequence 2, Appli
26	9	47.4	192	US-08-856-034-3	Sequence 3, Appli
27	9	47.4	192	US-08-856-034-8	Sequence 8, Appli

28 9 47.4 192 2 US-08-856-034-9 Sequence 9, Appli
29 9 47.4 192 3 US-08-471-057-13 Sequence 13, Appli
30 9 47.4 192 4 US-09-127-048-6 Sequence 6, Appli
31 9 47.4 192 4 US-09-127-048-7 Sequence 7, Appli
32 9 47.4 192 4 US-08-927-326-2 Sequence 2, Appli
33 9 47.4 192 4 US-08-927-326-3 Sequence 3, Appli
34 9 47.4 192 4 US-08-927-326-8 Sequence 8, Appli
35 9 47.4 192 4 US-08-927-326-9 Sequence 9, Appli
36 9 47.4 192 5 PCT-US95-04600-25 Sequence 25, Appli
37 9 47.4 221 1 US-08-616-732A-9 Sequence 9, Appli
38 9 47.4 221 4 US-09-037-742B-9 Sequence 9, Appli
39 6 31.6 120 4 US-09-134-001C-5332 Sequence 5332, Ap
40 6 31.6 154 4 US-09-397-787-16 Sequence 16, Appli
41 6 31.6 932 4 US-09-071-035-416 Sequence 416, App
42 6 31.6 969 4 US-09-071-035-414 Sequence 2, Appli
43 6 31.6 2165 1 US-08-514-975B-2 Sequence 2, Appli
44 6 31.6 2165 5 PCT-US95-12507-2 Sequence 20, Appli
45 5 26.3 5 1 US-08-798-897-20

ALIGNMENTS

RESULT 1
US-09-166-028-1
; Sequence 1, Application US/09166028
; Patent No. 6245885
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; TITLE OF INVENTION: REAGENTS AND METHODS
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/166,028
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic based on consensus sequence of Homo
; OTHER INFORMATION: sapiens, Mus musculus, and Rattus norvegicus
; NAME/KEY: VARIANT
; LOCATION: (6)...(10)
; OTHER INFORMATION: Xaa at 6 can be E or D; Xaa at 7 can be Q or H;
; OTHER INFORMATION: Xaa at 8 can be L or P; Xaa at 9 can be R or G;
; OTHER INFORMATION: Xaa at 10 can be S or G;
US-09-166-028-1

Query Match 73.7% Score 14; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGXXXXXGGPTSSEQI 19
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Db 1 MDGSGXXXXXGGPTSSEQI 19

RESULT 2
US-09-166-028-3
; Sequence 3, Application US/09166028
; Patent No. 6245885
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; TITLE OF INVENTION: REAGENTS AND METHODS
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/166,028
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

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; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-028-3

Query Match          47.4%; Score 9; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19

RESULT 3
US-09-166-028-4
; Sequence 4, Application US/09166028
; Patent No. 6245885
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/166,028
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-166-028-4

Query Match          47.4%; Score 9; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19

RESULT 4
US-09-166-028-5
; Sequence 5, Application US/09166028
; Patent No. 6245885
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/166,028
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-166-028-5

Query Match          47.4%; Score 9; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19

RESULT 5
US-08-798-897-21
; Sequence 21, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-798-897-21

Query Match          47.4%; Score 9; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
Db 6 GGPTSSEQI 14

RESULT 6
US-08-978-523-21
; Sequence 21, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483.0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-978-523-21

Query Match 47.4%; Score 9; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19

|||||

Db 6 GGPTSSEQI 14

RESULT 7

US-08-112-208C-2
Sequence 2, Application US/08112208C
Patent No. 5691179

GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/112.208C
FILING DATE: 26-AUG-1993
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-112-208C-2

Query Match 47.4%; Score 9; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19

|||||

Db 11 GGPTSSEQI 19

RESULT 8

US-08-112-208C-3
Sequence 3, Application US/08112208C
Patent No. 5691179

GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/112,208C
FILING DATE: 26-AUG-1993
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..192
OTHER INFORMATION: /note= "Protein sequence of murine Bax."
US-08-112-208C-3

Query Match

Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19

|||||

Db 11 GGPTSSEQI 19

RESULT 9

US-08-112-208C-8

Sequence 8, Application US/08112208C
Patent No. 5691179

GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; FILING DATE: US/08/112,208C
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 15726A-000610
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 192 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-112-208C-8

Query Match 47.4%; Score 9; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
|||||
DB 11 GGPTSSEQI 19

RESULT 10
US-08-112-208C-9
; Sequence 9, Application US/08112208C
; Patent No. 5691179
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/112,208C
FILING DATE: 26-AUG-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.

REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-112-208C-9

Query Match 47.4%; Score 9; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GGPTSSEQI 19
|||||
DB 11 GGPTSSEQI 19
RESULT 11
US-08-248-819A-2
; Sequence 2, Application US/08248819A
; Patent No. 5700638
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,819A
FILING DATE: 25-NAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-248-819A-2

Query Match 47.4%; Score 9; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
|||||
DB 11 GGPTSSEQI 19

RESULT 12
US-08-248-819A-3
; Sequence 3, Application US/08248819A
; Patent No. 5700638
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California

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; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,819A
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..192
; OTHER INFORMATION: /note= "Protein sequence of murine
; BAX."
US-08-248-819A-3

Query Match 47.4%; Score 9; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19

RESULT 13
US-08-248-819A-8
; Sequence 8, Application US/08248819A
; Patent No. 5700638
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Hourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,819A
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-248-819A-9

Query Match 47.4%; Score 9; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19
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; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-248-819A-8

Query Match 47.4%; Score 9; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19

RESULT 14
US-08-248-819A-9
; Sequence 9, Application US/08248819A
; Patent No. 5700638
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Hourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,819A
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-248-819A-9

Query Match 47.4%; Score 9; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSEQI 19
Db 11 GGPTSSEQI 19
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Query Match      47.4%; Score 9; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 11 GGPTSSEI 19
 Dp 11 GGPTSSEI 19

Search completed: January 7, 2003, 12:40:51
Job time : 11.2051 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2003, 12:27:38 ; Search time 23.8718 seconds
(without alignments)
163.997 Million cell updates/sec

Title: US-09-876-204-1
Perfect score: 78
Sequence: 1 MDGSCXXXXXGGPTSSEQI 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Query Length	ID	Description
1	69	88.5	24	11 Q8VHY7	Q8vhy7 mus musculus
2	67	85.9	24	4 Q8WXU1	Q8wxu1 homo sapien
3	67	85.9	164	4 Q9UQD6	Q9uqd6 homo sapien
4	67	85.9	179	4 Q9NYG7	Q9nyg7 homo sapien
5	58	74.4	192	6 Q8SQ43	Q8sq43 felis silve
6	41	52.6	315	17 Q8TIC5	Q8tic5 methanosarc
7	41	52.6	625	5 Q9NE37	Q9ne37 leishmania
8	40	51.3	487	3 Q05377	Q05377 saccharomyc
9	40	51.3	492	3 Q12317	Q12317 saccharomyc
10	40	51.3	528	3 Q05378	Q05378 saccharomyc
11	40	51.3	893	11 Q9NLI5	Q9nli5 mus musculus
12	39	50.0	248	16 Q9CG22	Q9cg22 lactococcus
13	39	50.0	677	5 Q9NNJ1	Q9nnj1 leishmania
14	39	50.0	1323	6 Q77509	Q77509 bos taurus
15	38	48.7	175	2 Q9WXD4	Q9wxd4 erwinia aph
16	38	48.7	297	4 Q9BHV5	Q9bhv5 homo sapien

17	38	48.7	312	4 Q9BV93	Q9bv93 homo sapien
18	38	48.7	487	2 Q51991	Q51991 pseudomonas
19	38	48.7	625	5 Q9V7S1	Q9v7s1 drosophila
20	38	48.7	871	5 O44358	O44358 nephiia cia
21	38	48.7	885	5 O61232	O61232 lymaea sta
22	38	48.7	1398	5 O77268	O77268 drosophila
23	38	48.7	1398	5 Q9W532	Q9w532 drosophila
24	38	48.7	1884	5 Q9NHW2	Q9nhw2 nephiia mad
25	38	48.7	2186	5 Q23984	Q23984 drosophila
26	38	48.7	2188	5 Q9VMD9	Q9vmd9 drosophila
27	38	48.7	2249	5 Q9NHW4	Q9nhw4 nephiia cia
28	37.5	48.1	927	2 Q9XAT8	Q9xat8 rhodococcus
29	37.5	48.1	1018	5 O17874	O17874 caenorhabdi
30	37	47.4	187	3 Q9C0V6	Q9c0v6 schizosacch
31	37	47.4	221	13 Q90X42	Q90x42 brachydanio
32	37	47.4	315	10 Q9FEU5	Q9feu5 pinus pinas
33	37	47.4	475	5 Q9VX11	Q9vxl1 drosophila
34	37	47.4	496	10 Q8SAU6	Q8sau6 oryza sativ
35	37	47.4	537	3 Q9UR24	Q9ur24 schizosacch
36	37	47.4	549	5 Q9VIR1	Q9vir1 drosophila
37	37	47.4	561	5 Q8T8V1	Q8t8v1 drosophila
38	37	47.4	583	3 Q9P768	Q9p768 schizosacch
39	37	47.4	589	5 Q9VM87	Q9vm87 drosophila
40	37	47.4	618	16 Q8ZPV6	Q8zpv6 salmonella
41	37	47.4	618	16 Q8Z6F3	Q8z6f3 salmonella
42	37	47.4	618	16 Q8XDW5	Q8xdw5 escherichia
43	37	47.4	636	6 Q9TUG3	Q9tug3 capra hircu
44	37	47.4	859	10 Q9FW70	Q9fw70 oryza sativ
45	37	47.4	884	5 O61543	O61543 drosophila

ALIGNMENTS

RESULT 1

Q8VHY7 ID Q8VHY7 PRELIMINARY: PRT: 24 AA.
AC Q8VHY7:
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Bcl2-associated X protein (Fragment).
GN BAX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Thornborrow E.C., Schwartzfarb E.M., Manfredi J.J.;
RT "A conserved intronic response element mediates direct p53-dependent
transcriptional activation of both the human and murine bax genes.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF339055; AAL73334.1; -.
FT NON_TER 24 24
SQ SEQUENCE 24 AA; 2326 MW; 998C7E8B7479A6CC CRC64;

Query Match 88.5%; Score 69; DB 11; Length 24;
Best Local Similarity 73.7%; Pred. No. 2.4e-06;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MDGSCXXXXXGGPTSSEQI 19

Db 1 MDGSGEQLGSGGPTSSEQI 19

RESULT 2

Q8WXU1 ID Q8WXU1 PRELIMINARY: PRT: 24 AA.
AC Q8WXU1:
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)

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DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE BCL2-associated X protein (Fragment).
GN BAX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Thornborrow E.C., Schwartzfarb E.M., Manfredi J.J.;
RT "A conserved intronic response element mediates direct p53-dependent
RT transcriptional activation of both the human and murine bax genes.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF339054; AAL73333.1; -.
FT ENM_TER 24 24
SQ SEQUENCE 24 AA; 2379 MW; 8C3D3E8B7479B798 CRC64;

Query Match 85.9%; Score 67; DB 4; Length 24;
Best Local Similarity 73.7%; Pred. No. 5.9e-06;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDGSGXXXXXXGGPTSSEQI 19
Db 1 MDGSGEQPRGGGPTSSEQI 19

RESULT 3
ID Q9UQD6 PRELIMINARY; PRT; 164 AA.
AC Q9UQD6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Bax epsilon.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue-BRAIN;
RC TISSUE-BRAIN;
RX MEDLINE=99120940; PubMed=9920818;
RA Shi B., Triebe D., Kajiji S., Iwata K.K., Bruskin A., Mahajna J.;
RT "Identification and characterization of baxepsilon, a novel bax
RT variant missing the BH2 and the transmembrane domains.";
RL Biochem. Biophys. Res. Commun. 254:779-785(1999).
DR EMBL; AF007826; AAD22706.1; -.
DR InterPro: IPR000712; BCL2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01259; BH3; 1.
SQ SEQUENCE 164 AA; 18129 MW; 12CCDB8073EF4C9E CRC64;

Query Match 85.9%; Score 67; DB 4; Length 164;
Best Local Similarity 73.7%; Pred. No. 4.6e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDGSGXXXXXXGGPTSSEQI 19
Db 1 MDGSGEQPRGGGPTSSEQI 19

RESULT 4
ID Q9NYG7 PRELIMINARY; PRT; 179 AA.
AC Q9NYG7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Bax-sigma.
```

```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20237095; PubMed=10772918;
RX Schmitt E., Paquet C., Beauchemin M., Dever-Bertrand J., Bertrand R.;
RT "Characterization of bax-sigma, a cell death-inducing isoform of
RT Bax.";
RL Biochem. Biophys. Res. Commun. 270:868-879(2000).
DR EMBL; AF247393; AAF71267.1; -.
DR HSSP; Q07817; IMAZ.
DR InterPro: IPR000712; BCL2_BH.
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01259; BH3; 1.
SQ SEQUENCE 179 AA; 19718 MW; 5802B0AC73B2EACE CRC64;

Query Match 85.9%; Score 67; DB 4; Length 179;
Best Local Similarity 73.7%; Pred. No. 5e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDGSGXXXXXXGGPTSSEQI 19
Db 1 MDGSGEQPRGGGPTSSEQI 19

RESULT 5
ID Q8SQ43 PRELIMINARY; PRT; 192 AA.
AC Q8SQ43;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Bax-protein.
GN BAX.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamazaki J., Oguma K., Kano R., Hasegawa A.;
RT "molecular cloning of feline bcl-2 family.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB080724; BAB85810.1; -.
SQ SEQUENCE 192 AA; 21283 MW; 852D271AE86923FB CRC64;

Query Match 74.4%; Score 58; DB 6; Length 192;
Best Local Similarity 68.4%; Pred. No. 0.003;
Matches 13; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 MDGSGXXXXXXGGPTSSEQI 19
Db 1 MDGSGEQPRGGGPTSSEQI 19

RESULT 6
ID Q8TIC5 PRELIMINARY; PRT; 315 AA.
AC Q8TIC5;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Predicted protein.
GN MA4230.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
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OX NCB1_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., MacDonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Alnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R.,
RA Linton D., McKean P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderley R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL: A011134; AAC07575.1; -.
KW Complete proteome.
SQ SEQUENCE 315 AA; 34004 MW; 3649A8CBE8784486 CRC64;

Query Match
Best Local Similarity 52.6%; Score 41; DB 17; Length 315;
Matches B: Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 GSGXXXXXGPTSS 16
DB 249 GAGGALGGPTSS 262

RESULT 7
Q9NE37 PRELIMINARY; PRT; 625 AA.
AC Q9NE37;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Possible ATP-dependent RNA helicase.
GN L6793.10;
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCB1_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIDLIN;
RA Zimmermann W., Harris D., Ivens A.C., Quail M., Rajandream M.A.,
RA Barrell B.G.;
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIDLIN;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL: AL354513; CAB89599.1; -.
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR000629; DEAD_box.
DR InterPro: IPR001650; Helicase_C.
DR pfam: PF00270; DEAD.
DR pfam: PF00271; helicase_C; 1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELIC; 1.
DR PROSITE: PS00039; DEAD_ATP_HELICASE; UNKNOWN_1.
DR ATP-binding; Helicase.
SQ SEQUENCE 625 AA; 66776 MW; 01D457D7F4FEB8B5 CRC64;

Query Match
Best Local Similarity 52.6%; Score 41; DB 5; Length 625;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 4 SGXXXXXXGPTSS 16
DB 278 SGSTGAAGGPTSS 290

RESULT 8
Q05377 PRELIMINARY; PRT; 487 AA.
AC Q05377;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chromosome XV DNA (44 kb fragment).
GN MSB4 AND YOL112W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCB1_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96076631; PubMed=7502582;
RA Vandenbol M., Durand P., Portetelle D., Hilger F.;
RT "Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV
including the Tyl-H3 retrotransposon, the sufl(+) frameshift
suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-1a and a
delta element.";
RL Yeast 11:1069-1075(1995).
DR EMBL: Z48149; CAA88149.1; -.
DR SGD: S0005472; MSB4.
DR InterPro: IPR000195; RadCAP_TBC.
DR pfam: PF00566; TBC; 1.
DR SMART: SM00164; TBC; 1.
DR SEQUENCE 487 AA; 5631 MW; B4FCF5632F7711F CRC64;

Query Match
Best Local Similarity 51.3%; Score 40; DB 3; Length 487;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDGSGXXXXXGPTSS 18
DB 310 MNGNGSTQDISGPASGFE 327

RESULT 9
Q12317 PRELIMINARY; PRT; 492 AA.
AC Q12317;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chromosome XV reading frame ORF YOL112W.
GN MSB4 OR YOL112W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCB1_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Durand P., Hilger F., Portetelle D., Vandenbol M.;
RL Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
MIPS:
RP Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96076631; PubMed=7502582;
RA Vandenbol M., Durand P., Portetelle D., Hilger F.;
RT "Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV
including the Tyl-H3 retrotransposon, the sufl(+) frameshift
suppressor gene for tRNA-Gly, the yeast transfer RNA-Thr-1a and a
delta element.";

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN:
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RT Genome Res. 8:135-145(1998).
DR EMBL: AL160371; CAC00219.2; -.
SQ SEQUENCE 677 AA; 71562 MW; 4FE7D3D13E56C310 CRC64;

Query Match 50.0%; Score 39; DB 5; Length 677;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 8; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 3 GSGGXXXXGGPTSSFOI 18
DB 528 GSGGCVLDGGPTDAMQ 543

RESULT 14
ID 077509 PRELIMINARY: PRT; 1323 AA.
AC 077509;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Submaxillary mucin (Fragment).
GN BSM2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99011416; PubMed=9792811;
RA Jiang W., Wollach J.T., Gupta D., Bhavananan V.P.;
RT "Sequence of a second gene encoding bovine submaxillary mucin:
RT implication for mucin heterogeneity and cloning.";
RL Biochem. Biophys. Res. Commun. 251:550-556(1998).
DR EMBL: AF019298; AAC72492.1; -.
DR InterPro: IPR000359; Cys_knot.
DR InterPro: IPR001007; VWF_C.
DR Pfam: PF00007; Cys_knot; 1.
DR SMART: SM00041; CT; 1.
DR SMART: SM00214; VWC; 1.
DR PROSITE: PS01185; CTCK_1; 1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS01208; VWF_C; 1.
FT NON_TER 1
SQ SEQUENCE 1323 AA; 133693 MW; D2C71C14968B96A8 CRC64;

Query Match 50.0%; Score 39; DB 6; Length 1323;
Best Local Similarity 38.9%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 2 DSGGXXXXGGPTSSFOI 19
DB 271 EGSGETGTAGPTRTTRI 288

RESULT 15
ID 09WXD4 PRELIMINARY: PRT; 175 AA.
AC 09WXD4;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Eafa.
GN Eafa.
OS Erwinia aphidicola.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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OC Erwinia.
OX NCBI_TaxID=68334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IAM14479;
RA Harada H., Ishikawa H.;
RT "Sugar induced 17 kDa surface protein of Erwinia aphidicola is
RT homologous to major fimbrial subunit of uropathogenic
RT enterobacteria.";
RL Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB019366; BAA/6627.1; -.
DR InterPro: IPR000259; Fimbrial.
DR Pfam: PF00419; Fimbrial; 1.
SQ SEQUENCE 175 AA; 17805 MW; 8AA03577A5E171DB CRC64;

Query Match 48.7%; Score 38; DB 2; Length 175;
Best Local Similarity 38.9%; Pred. No. 20;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 DSGGXXXXGGPTSSFOI 19
DB 117 DSGGKIEIGPTTAOTL 134
```

Search completed: January 7, 2003, 12:30:47
Job time : 25.8718 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:25:07 : Search time 7.69231 Seconds
(without alignments)
107.838 Million cell updates/sec

Title: US-09-876-204-3

Perfect score: 106

Sequence: 1 MDGSGEPGCGPTSSSEQIM 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	100.0	143	1 BAXD_HUMAN	P55269 homo sapien
2	106	100.0	192	1 BAXA_BOVIN	002703 bos taurus
3	106	100.0	192	1 BAXA_HUMAN	007812 homo sapien
4	106	100.0	218	1 BAXB_HUMAN	007814 homo sapien
5	89	84.0	192	1 BAXA_RAT	063690 ratu
6	83	78.3	192	1 BAXA_MOUSE	007813 mus musculu
7	65	61.3	41	1 BAXC_HUMAN	007815 mus musculu
8	52	49.1	475	1 MORD_RHIME	052964 rhizobium m
9	47	44.3	397	1 KPRP_MESCR	P27774 mesembryant
10	46.5	43.9	321	1 ISP_BACCS	P29140 bacillus cl
11	46	43.4	482	1 EIBL_ADE12	P04491 human adeno
12	46	43.4	654	1 HSTO_HYDMA	005944 hydra magni
13	45.5	42.9	434	1 VABR_BORBU	051120 borfella bu
14	45	42.5	351	1 E2BB_HUMAN	P49770 homo sapien
15	44.5	42.0	484	1 MEC2_MOUSE	092246 mus musculu
16	44.5	42.0	492	1 MEC2_RAT	000566 ratu
17	44	41.5	276	1 FLIJ_CAUCR	P02969 caulobacter
18	44	41.5	402	1 KPRP_SPTOL	P09539 splachia ol
19	44	41.5	404	1 KPRP_WHEAT	P26302 triticum ae
20	44	41.5	511	1 FASP_MOUSE	0911x mus musculu
21	44	41.5	571	1 IF2_TRETH	P48515 thermus the
22	44	41.5	1241	1 PER_DROPS	P12348 drosophila
23	44	41.5	1848	1 CCAA_DROME	P91645 drosophila
24	43	40.6	340	1 ERMA_ARTS3	P09891 artinobacte
25	43	40.6	486	1 MEC2_HUMAN	P51608 homo sapien
26	43	40.6	501	1 IRK3_HUMAN	P48549 homo sapien
27	43	40.6	507	1 CP5G_CANTR	P30608 candida tro
28	43	40.6	524	1 CP5F_CANTR	P30608 candida tro
29	43	40.6	1752	1 RPA1_SCHPO	P36594 schizosacch
30	42.5	40.1	460	1 VABT_METMA	060187 methanosarc
31	42.5	40.1	3511	1 MY15_MOUSE	Q94224 mus musculu
32	42	39.6	319	1 K6PF_LACDE	P80019 lactobacilli
33	42	39.6	347	1 UTR2_YEAST	P32623 saccharomyc

34	42	39.6	440	1 PD46_CAEEL	O11067 caenorhabdi
35	42	39.6	501	1 IRK3_MOUSE	P35562 mus musculu
36	42	39.6	1150	1 APMD_PIG	P12021 sus scrofa
37	42	39.6	1171	1 DPOL_HSVT2	Q9YUS2 herpesvirus
38	41.5	39.2	1505	1 CUL1_HUMAN	P39880 homo sapien
39	41	38.7	147	1 HOLC_ECOLI	P28905 escherichia
40	41	38.7	216	1 VP2_CAVB2	P54092 chicken ane
41	41	38.7	216	1 VP2_CAVB2	P54092 chicken ane
42	41	38.7	216	1 VP2_CAVC1	Q99151 chicken ane
43	41	38.7	322	1 K6P1_TRETH	P21777 thermus the
44	41	38.7	329	1 K6PF_DEIRA	Q97W11 deinococcus
45	41	38.7	476	1 HLX1_MOUSE	O61670 mus musculu

ALIGNMENTS

RESULT 1	BAXD_HUMAN	STANDARD:	PRT:	143 AA.
ID	BAXD_HUMAN			
AC	P55269;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	BAX protein, cytoplasmic isoform delta.			
GN	BAX.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_Taxid:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:9531797; PubMed=7607685;			
RA	Apte S.S., Matei M.-G., Olsen B.R.;			
RT	"Mapping of the human BAX gene to chromosome 19q13.3-q13.4 and			
RT	isolation of a novel alternatively spliced transcript, BAX delta.";			
RL	Genomics 26:592-594(1995).			
CC	- SUBCELLULAR LOCATION: Cytoplasmic (Potential).			
CC	- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE			
CC	CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY			
CC	ALTERNATIVE SPLICING.			
CC	- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.			
CC	- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.			
CC	- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC				
CC	EMBL: U19599; AAC50142.1; -			
DR	Genew: HGNC:959; BAX.			
DR	MTM: 600040; -			
DR	InterPro: IPR002475; BCL2_family.			
DR	InterPro: IPR000712; Bcl2_BH.			
DR	Pfam: PF00452; Bcl-2; 1.			
DR	SMART: SM00337; BCL; 1.			
DR	PROSITE: PS01080; BH1; 1.			
DR	PROSITE: PS01258; BH2; 1.			
DR	PROSITE: PS50062; BCL2_FAMILY; 1.			
KW	Apoptosis; Alternative splicing.			
KW	Apoptosis; Alternative splicing.			
FT	DOMAIN 49..69			
FT	DOMAIN 101..116			
SO	SEQUENCE 143 AA; 15772 MW; BADEAD71D06A75AB CRC64;			
Query Match	100.0%;	Score 106;	DB 1;	Length 143;
Best Local Similarity	100.0%;	Pred. No. 3e-08;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1 MDGSGEPGCGPTSSSEQIM 20			

Db 1 MDGSGEOPRGCGPTSSEQIM 20

RESULT 2
BAXA_BOVIN STANDARD: PRT: 192 AA.

AC 002703;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=Holstein; TISSUE=Thymus;
RX MEDLINE=98162580; PubMed=9501056;

RA Reyes R.A., Cockerell G.L.,
RT "Increased ratio of bcl-2/bax expression is associated with bovine leukemia virus-induced leukemogenesis in cattle."
RL Virology 242:184-192(1998).

CC -1 FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C, ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE CESSATION OF SPERM PRODUCTION (BY SIMILARITY).

CC -1 SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2, E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1 (BY SIMILARITY).

CC -1 SUBCELLULAR LOCATION: Membrane-bound (by similarity).
CC -1 ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE SPLICING.

CC -1 DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).
CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1 SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

CC -----
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CC -----

DR EMBL: U92569; AAC48806.1; -
DR HSSP: Q07817; IMA2.
DR InterPro: IPR002475; BCL2 family.
DR InterPro: IPR000712; BCL2_BH.

DR Pfam: PF00452; BCL-2; 1.
DR SMART: SM00357; BCL; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS00062; BCL2_FAMILY; 1.
DR Apoptosis; Transmembrane; Alternative splicing.

FT DOMAIN 59 73 BH3.
FT DOMAIN 98 118 BH1.
FT DOMAIN 150 165 BH2.
FT TRANSMEM 172 192 POTENTIAL.
SQ SEQUENCE 192 AA; 21259 MW; 6B45DBABF1D5F78E CRC64;

Query Match 100.0%; Score 106; DB 1; Length 192;

Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDGSGEOPRGCGPTSSEQIM 20
Db 1 MDGSGEOPRGCGPTSSEQIM 20

RESULT 3
BAXA_HUMAN STANDARD: PRT: 192 AA.

AC 007812;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=93364978; PubMed=8358790;
RA Olvay Z.N., Millman C.L., Korsmeyer S.J.;

RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates programmed cell death."
RL Cell 74:609-619(1993).

RN [2]
RP MOTAGNESIS, AND FUNCTION OF BH3 DOMAIN.
RX MEDLINE=96091131; PubMed=8521816;

RA Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,
RA Elangovan B., Chinnadurai G., Lutz R.J.;

RT "A conserved domain in Bax, distinct from BH1 and BH2, mediates cell death and protein binding functions."
RL EMBO J. 14:5589-5596(1995).

RN [3]
RP VARIANT PLASMACYTOMA GLO-11, VARIANT T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ARG-67, AND VARIANT BURKITT LYMPHOMA VAL-108.
RX MEDLINE=98200607; PubMed=9531611;
RA Meljertink J.P.P., Mensink E.J.B.W., Wang K., Sedlak T.W.,
RA Sloetjes A.W., de Witte T., Waksman G., Korsmeyer S.J.;

RT "Hematopoietic malignancies demonstrate loss-of-function mutations of BAX."
RL Blood 91:2991-2997(1998).

CC -1 FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C, ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.

CC -1 SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2, E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.

CC -1 SUBCELLULAR LOCATION: Membrane-bound.
CC -1 ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.

CC -1 TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC -1 DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1 DISEASE: Defects in BAX are found in some cell lines from hematopoietic malignancies as T-cell acute lymphoblastic leukemia, Burkitt lymphoma, and plasmacytoma.

CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1 SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

CC -----
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CC or send an email to license@isb.sib.ch).
CC -----
CC EMBL: L22473; AAA03619.1; -.
CC DR PIR: A47538; A47538.
CC DR HSSP; Q07817; 1MAZ.
CC DR Genew; HGNC:959; BAX.
CC DR MIM; 600040; -.
CC DR InterPro: IPR002475; BCL2_family.
CC DR InterPro: IPR000712; BCL2_BH.
CC DR Pfam; PF00452; BCL-2; 1.
CC DR SMART; SM00337; BCL_1.
CC DR PROSITE; PS50062; BCL2_FAMILY; 1.
CC DR PROSITE; PS01080; BH1; 1.
CC DR PROSITE; PS01258; BH2; 1.
CC DR PROSITE; PS01259; BH3; 1.
CC KW Apoptosis; Anti-oncogene; Transmembrane; Alternative splicing;
CC KM Disease mutation.
CC FT DOMAIN 59 73 BH3.
CC FT DOMAIN 98 118 BH1.
CC FT DOMAIN 150 165 BH2.
CC FT TRANSMEM 172 192 POTENTIAL.
CC FT VARIANT 11 11 G->E (IN PLASMACYOMA).
CC FT VARIANT 67 67 /FTID=VAR_013575.
CC FT LEUKEMIA: LOSS OF HETERODIMERIZATION WITH
CC FT BCL-2 OR BCL-X(L)).
CC FT VARIANT 108 108 /FTID=VAR_007809.
CC FT G->V (IN BURKITT LYMPHOMA; LOSS OF
CC FT HOMODIMERIZATION).
CC FT /FTID=VAR_013576.
CC SQ SEQUENCE 192 AA; 21184 MM; 6C0CDB0A7DEE4994 CRC64;
CC
CC Query Match 100.0%; Score 106; DB 1; Length 192;
CC Best Local Similarity 100.0%; Pctd. No. 4,1e-08;
CC Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Oy 1 MDGSGEOPRGCGPTSSFOIM 20
CC Db 1 MDGSGEOPRGCGPTSSFOIM 20
CC ||||||||||||||||
CC
CC RESULT 4
CC BAXB_HUMAN STANDARD: PRT: 218 AA.
CC ID BAXB_HUMAN
CC AC Q07814;
CC DT 01-FEB-1995 (Rel. 31, Created)
CC DT 01-FEB-1995 (Rel. 31, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Apoptosis regulator BAX, cytoplasmic isoform beta.
CC GN BAX.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CC OX NCBI_TaxID=9606;
CC RX MEDLINE=93364978; PubMed=8358790;
CC RC TISSUE=B-cell;
CC RA Olvera Z.N., Millman C.L., Korsmeyer S.J.;
CC RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
CC RL Cell 74:609-619(1993).
CC CC -I- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
CC HOMOLOG E1B 19K PROTEIN.
CC CC -I- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC CC -I- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
CC ALTERNATIVE SPLICING.

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CC -I- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC -I- DOMAIN: INTRACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb.ch).
CC -----
CC EMBL: L22474; AAA03620.1; -.
CC PIR: B47538; B47538.
CC HSSP: Q07817; 1MAZ.
CC Genew: HGNC:959; BAX.
CC MIM: 600040; -.
CC DR InterPro: IPR002475; BCL2_family.
CC DR InterPro: IPR000712; BCL2_BH.
CC DR Pfam: PF00452; BCL-2; 1.
CC DR SMART: SM00337; BCL; 1.
CC DR PROSITE: PS01080; BH1; 1.
CC DR PROSITE: PS01258; BH2; 1.
CC DR PROSITE: PS01259; BH3; 1.
CC DR PROSITE: PS50062; BCL2_FAMILY; 1.
CC KW Apoptosis; Alternative splicing.
CC FT DOMAIN 59 73 BH3.
CC FT DOMAIN 98 118 BH1.
CC FT DOMAIN 150 165 BH2.
CC SO SEQUENCE 218 AA; 24220 MW; F69DCD70F960192F CRC64;

Query Match 100.0%; Score 106; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGGGPTSSQIM 20
DB 1 MDGSGEOPRGGGPTSSQIM 20
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|||||

RESULT 5
BAXA__RAT STANDARD: PRT; 192 AA.
ID BAXA_RAT
AC 063690; 062995; 064383;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
OS BAX.
GN Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96178771; PubMed=8600029;
RA Han J., Sabbatini P., Perez D., Rao L., Modha D., White E.;
RT "The E1B 19K protein blocks apoptosis by interacting with and
RT inhibiting the p53-inducible and death-promoting Bax protein.";
RL Genes Dev. 10:461-477(1996).
RN [2]
RP SEQUENCE OF 75-192 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97147318; PubMed=8994423;
RA Madison D.L., Pfeiffer S.E.;
RT "Cloning of the 3' end of rat bax-alpha and corresponding
RT developmental down-regulation in differentiating primary, cultured

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RT oligodendrocytes."
RL Neurosci. Lett. 220:183-186(1996).
RN [3]
RP SEQUENCE OF 37-169 FROM N.A.
RC STRAIN-Sprague-Dawley: TISSUE-Ovary:
RX MEDLINE=95129487; PubMed=7828536.
RA Tilly J.L., Tilly K.L., Kenton M.L., Johnson A.L.;
RT "Expression of members of the bcl-2 gene family in the immature rat
RT ovary: equine chorionic gonadotrophin-mediated inhibition of granulosa
RT cell apoptosis is associated with decreased bax and constitutive
RT bcl-2 and bcl-x-long messenger ribonucleic acid levels."
RL Endocrinology 136:232-241(1995)
CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
CC HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC -1- SUBCELLULAR LOCATION: Membrane-bound.
CC -1- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO
CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES. WITH
CC HIGHEST LEVELS IN THE TESTIS AND OVARY.
CC -1- DOMAIN: INTRACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOMOLOGY 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOMOLOGY 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOMOLOGY 3 (BH3) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL: U49729; AAC26327.1; -
DR EMBL: U59184; AAC52988.1; -
DR EMBL: U32098; AAA75200.1; -
DR EMBL: S76511; AAC60700.2; -
DR HSSP: P53563; IAF3.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
KW Apoptosis; Transmembrane; Alternative splicing.
FT DOMAIN 59 73 BH3.
FT DOMAIN 98 118 BH1.
FT DOMAIN 150 165 BH2.
FT TRANSMEM 172 192 POTENTIAL.
FT CONFLICT 72 72 S -> N (IN REF. 3).
FT CONFLICT 76 76 L -> M (IN REF. 2).
FT CONFLICT 126 126 C -> Y (IN REF. 2).
FT CONFLICT 149 149 L -> F (IN REF. 2).
FT CONFLICT 159 159 D -> E (IN REF. 1).
KW Apoptosis; Transmembrane; Alternative splicing.
SQ SEQUENCE 192 AA; 21350 MW; 7B3CD198D56DF589 CRC64;

Query Match Score 89; DB 1; Length 192;
Best Local Similarity 90.0%; Pred. No. 9, 8e-06;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 6
BAXA_MOUSE
ID BAXA_MOUSE STANDARD; PRT; 192 AA.
AC 007813;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X DBA/2;
RX MEDLINE=93364978; PubMed=8358790;
RA Oliva J.N., Millman C.L., Korsmeyer S.J.;
RT "bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
RT accelerates programmed cell death."
RL Cell 74:609-619(1993)
CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
CC HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY
CC LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE
CC CESSATION OF SPERM PRODUCTION.
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC -1- SUBCELLULAR LOCATION: Membrane-bound.
CC -1- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO
CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC -1- DOMAIN: INTRACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOMOLOGY 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOMOLOGY 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOMOLOGY 3 (BH3) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL: L22472; AAA3622.1; -
DR HSSP: P53563; IAF3.
DR MGD: MGI:99702; Bax.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
KW Apoptosis; Transmembrane; Alternative splicing.
FT DOMAIN 59 73 BH3.
FT DOMAIN 98 118 BH1.
FT DOMAIN 150 165 BH2.
FT TRANSMEM 172 192 POTENTIAL.
SQ SEQUENCE 192 AA; 21394 MW; D2E0B3566579FAFV CRC64;

Query Match Score 83; DB 1; Length 192;
Best Local Similarity 85.0%; Pred. No. 6, 8e-05;

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGCGPTSSQIM 20
 Db 1 MDGSGEOLGSGGPTSSQIM 20

RESULT 7

BAXC_HUMAN
 ID BAXC_HUMAN STANDARD; PRT; 41 AA.
 AC 007815;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE BAX protein, cytoplasmic isoform gamma.
 GN BAX.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RA MEDLINE=93364978; PubMed=8358790;
 RA Olvai Z.N., Millman C.L., Korsmeyer S.J.;
 RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
 RT accelerates programmed cell death."
 RL Cell 74:609-619(1993).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
 CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
 CC ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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DR EMBL: L22475; AAA03621.1; -
 DR Genew: HNCN:959; BAX.
 DR MIM: 600040; -
 DR Apoptosis: Alternative splicing;
 KW Apoptosis: 41 AA; 4678 MW; D94639AAB927859 CRC64;
 SQ SEQUENCE

Query Match 61.3%; Score 65; DB 1; Length 41;
 Best Local Similarity 72.2%; Pred. No. 0.0046;
 Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGCGPTSSQ 18
 Db 1 MDGSGEOPRGGSRSLEQ 18

RESULT 8

MOTD_RHIME
 ID MOTD_RHIME STANDARD; PRT; 475 AA.
 AC 052964;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Chemotaxis motD protein (Motility protein D).
 GN MOTD.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RUI1/001;

RX MEDLINE=97474264; PubMed=9335288;
 RA Platzer J., Sterr W., Hausmann M., Schmitt R.;
 RT "three genes of a motility operon and their role in flagellar rotary
 RT speed variation in Rhizobium meliloti."
 RL J. Bacteriol. 179:6391-6399(1997).

CC -1- FUNCTION: REQUIRED FOR THE ROTATION OF THE FLAGELLAR MOTOR.
 CC HAS A POSITIVE EFFECT AS FLAGELLAR ROTATION INCREASES WHEN AN
 CC EXCESS OF MOTD IS PRESENT.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH THE INNER
 CC SURFACE OF THE MOTOR (PROBABLE).

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DR EMBL: LA9337; AAB81410.1; -
 DR Chemotaxis; Flagella; Flagellar rotation.
 FT DOMAIN 413 416 POLY-GLY.
 SQ SEQUENCE 475 AA; 48842 MW; 9CD14F5F44ABEE93 CRC64;

Query Match 49.1%; Score 52; DB 1; Length 475;
 Best Local Similarity 52.9%; Pred. No. 3.8;
 Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 DSGEOPRGCGPTSSQ 18
 Db 435 DSGEOPRGCGRATER 451

RESULT 9

KPPR_MESCR
 ID KPPR_MESCR STANDARD; PRT; 397 AA.
 AC P27774;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phosphoribulokinase, chloroplast precursor (EC 2.7.1.19)
 DE (phosphoribulokinase) (PRKASE) (PRK).
 OS Mesembryanthemum crystallinum (common ice plant).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.
 OX NCBI_TaxID=3544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Michalowski C.B., Derocher F.J., Bohnert H.J., Salvucci M.E.;
 RL Submitted (XXX-1991) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + D-ribulose 5-phosphate = ADP + D-
 CC ribulose 1,5-bisphosphate.
 CC -1- ENZYME REGULATION: LIGHT REGULATED VIA THIORDOXIN BY REVERSIBLE
 CC OXIDATION/REDUCTION OF SULFHYDRYL/DISULFIDE GROUPS.
 CC -1- PATHWAY: Calvin cycle.
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHORIBULOKINASE FAMILY.
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DR EMBL: M73707; AAA33034.1; -
 DR InterPro: IPR001324; PRK.
 DR Pfam: PF00485; PRK.1.
 DR PRINTS: PR00478; PHOSPHORIBULOKINASE.
 DR PROSITE: PS00567; PHOSPHORIBULOKINASE; 1.
 KW Transferase; Kinase; Chloroplast; Transit peptide; Calvin cycle;
 KW ATP-binding; Photosynthesis.

FT TRANSIT 1 44 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 45 397 PHOSPHORIBULOKINASE.
 FT DISULFID 62 101 BY SIMILARITY.
 SQ SEQUENCE 397 AA; 44114 MW; 88DC418E211EC975 CRC64;

Query Match 44.38; Score 47; DB 1; Length 397;
 Best Local Similarity 52.98; Pred. No. 16;
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 3 GSGEOPRGCGPTSSEQ 19
 DB 77 GAAPPPGCGNPDSTWTL 93

RESULT 10
 ISP_BACCS STANDARD; PRT; 321 AA.
 AC P29140;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Intracellular alkaline protease (EC 3.4.21.-).
 OS Bacillus clausii.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=79880;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=221 / ATCC 21522 / JCM 9139 / DSM 2512;
 RA Kato C., Nakano Y., Yamamoto M., Horikoshi K.;
 RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
 CC -----
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CC EMBL: D10730; BAA01573.1; -
 DR PIR: S27501; S27501.
 DR HSSP: P00782; I501.
 DR MEROPS: S08.030; -
 DR InterPro: IPR000209; Peptidase_S8.
 DR Pfam: PF00082; Peptidase_S8; 1.
 DR PRINTS: PR00723; SUBTILISIN.
 DR PROSITE: PS00136; SUBTILASE_ASP; 1.
 DR PROSITE: PS00137; SUBTILASE_HIS; 1.
 DR PROSITE: PS00138; SUBTILASE_SER; 1.
 KW Hydrolyase; serine protease.
 FT ACT_SITE 49 49 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 86 86 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 250 250 CHARGE RELAY SYSTEM (BY SIMILARITY).
 SQ SEQUENCE 321 AA; 33747 MW; 621168D9F1044026 CRC64;

Query Match 43.9%; Score 46.5; DB 1; Length 321;
 Best Local Similarity 30.2%; Pred. No. 15;
 Matches 13; Conservative 3; Mismatches 2; Indels 25; Gaps 2;

OY 2 DSGSEOPRGCGPTSSEQ 19
 DB 121 DSGSEGMWIAKAIKRYAVDMRGKGEQMRITMSLGGPTDSEEL 163

RESULT 11
 EIBL_ADEI2 STANDARD; PRT; 482 AA.
 AC P04491;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE E1B protein, large T-antigen.

OS Human adenovirus type 12.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=28282;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=82105565; PubMed=6275367;
 RA Kimura T., Sawada Y., Shinawawa M., Shimizu Y., Shiroki K.,
 RA Shimizu H., Sugisaki H., Takamami M., Uemizu Y., Fujinaga K.;
 RT "Nucleotide sequence of the transforming early region E1b of
 RT adenovirus type 12 DNA: structure and gene organization, and
 RT comparison with those of adenovirus type 5 DNA.";
 RL Nucleic Acids Res. 9:6571-6589(1981).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82115327; PubMed=7326748;
 RA Bos J.L., Polder L.J., Bernards R., Schrier P.I., van den Elsen P.J.,
 RA van der Eb A.J., van Ormondt H.;
 RT "The 2.2 kb E1b mRNA of human Ad12 and Ad5 codes for two tumor
 RT antigens starting at different AUG triplets.";
 RL Cell 27:121-131(1981).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94076430; PubMed=8254750;
 RA Sprengel J., Schmitz B., Heuss-Weitzel D., Zock C., Doerfler W.;
 RT "Nucleotide sequence of human adenovirus type 12 DNA: comparative
 RT functional analysis.";
 RL J. Virol. 68:379-389(1994).

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CC EMBL: V00004; CAA23407.1; -
 DR EMBL: X73487; CAA51879.1; -
 DR PIR: A03812; ERAD24.
 DR PIR: S33930; S33930.
 DR InterPro: IPR002612; AdenoE1B_55kDa.
 DR Pfam: PF01696; Adeno_E1B_55k; 1.
 KW Early protein.
 SQ SEQUENCE 482 AA; 53935 MW; 359E8082B7EF3659 CRC64;

Query Match 43.4%; Score 46; DB 1; Length 482;
 Best Local Similarity 47.1%; Pred. No. 27;
 Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 2 DSGSEOPRGCGPTSSEQ 18
 DB 50 EGGAEPGCGGEVNMEO 66

RESULT 12
 HS70_HYDMA STANDARD; PRT; 654 AA.
 ID HS70_HYDMA
 AC 005944;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Heat shock 70 kDa protein.
 GN HSP70.1.
 OS Hydra magnipapillata (Hydra).
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroidae; Anthomedusae;
 OC Hydrozoa; Hydra.
 OX NCBI_TaxID=6085;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93130891; PubMed=1483453;
 RA Gellner K., Praetzel G., Bosch T.C.G.;
 RT "Cloning and expression of a heat-inducible hsp70 gene in two species
 RT of Hydra which differ in their stress response.";

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RL Eur. J. Biochem. 210:683-691(1992).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
CC -----
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CC -----
CC EMBL: M84019; AAA29213.1; -.
CC PIR: S27004; S27004.
CC DR HSP: P08109; 1CKR.
CC DR InterPro: IPR001023; Hsp70.
CC DR Pfam: PF00012; HSP70_1.
CC DR PRINTS: PR00301; HEATSHOCK70.
CC DR PRODOM: PD000089; HSP70_1.
CC DR PROSITE: PS00297; HSP70_1; 1.
CC DR PROSITE: PS00329; HSP70_2; 1.
CC DR PROSITE: PS01036; HSP70_3; 1.
CC KW ATP-binding; Heat shock.
CC SQ SEQUENCE 654 AA; 71467 MW; 5BC1EA4BA1E640FB CRC64;

Query Match 43.4%; Score 46; DB 1; Length 654;
Best Local Similarity 52.9%; Pred. No. 36;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 MDGSGEOPRGGPTSEQIM 17
DB 636 MPDGSKASSGPTIE 652

RESULT 13
VATB_BORBU
ID VATB_BORBU STANDARD; PRT; 434 AA.
AC 051120;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE V-type ATP synthase beta chain (EC 3.6.3.14) (V-type ATPase subunit
DE B).
GN ATPB OR BB0093.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria: Spirochaetales: Spirochaetaceae: Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Castjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty J., Tomb J.-F., Fleischmann R.D., Richardson S.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman C.,
RA Ulterback T., Matthey L., McDonald L., Artlich P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, Borrelia
RT burgdorferi."
RL Nature 390:580-586(1997).
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE. THE V-TYPE BETA CHAIN IS A
CC REGULATORY SUBUNIT.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(++) (In) = ADP + phosphate +
CC H(++) (Out).
CC -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
CC -----
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CC -----
CC EMBL: AE001122; AAC66484.1; -.
CC DR TIGR: BB0093; -.
CC DR InterPro: IPR004100; ATPase_a/bN.
CC DR InterPro: IPR000194; ATPase_a/bcentre.
CC DR Pfam: PF00006; ATP-synt_ab; 1.
CC DR Pfam: PF02874; ATP-synt_ab_N; 1.
CC DR PROSITE: PS00152; ATPASE_ALPHA_BETA; FALSE_NEG.
CC KW Hydrolyase; ATP synthesis; Hydrogen ion transport; Complete proteome.
CC SQ SEQUENCE 434 AA; 48026 MW; 5FF0293DBD91361B CRC64;

Query Match 42.9%; Score 45.5; DB 1; Length 434;
Best Local Similarity 47.4%; Pred. No. 28;
Matches 9; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 2 DSGSGEOPRGGPTSEQIM 20
DB 88 DSGG-NPRDGPISLDNLI 105

RESULT 14
E2BB_HUMAN
ID E2BB_HUMAN STANDARD; PRT; 351 AA.
AC P49770; O43201;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Translation initiation factor eIF-2B beta subunit (eIF-2B GDP-GTP
DE exchange factor) (S20115) (S2011115).
CN EIF2B2 OR EIF2B.
OS Homo sapiens (human).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RA TISSUE-Brain;
RA Yu W., Sarginson J., Gibbs R.A.;
RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE=95319502; PubMed=7596406;
RA Sherrington R., Rogaev E.I., Liang Y., Rogaeva E.A., Levesque G.,
RA Ikeda M., Chi H., Lin C., Holman K., Tsuda T., Mar L.,
RA Foncin J.-F., Bruni A.C., Montesi M.P., Sorbi S., Rainero I.,
RA Pinessi L., Nee L., Chumakov I., Pollen D., Brookes A.,
RA Sansau P., Polinsky R.J., Masco W., da Silva H.A.R., Haines J.L.,
RA Perleac-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E.,
RA Romanes J.M., St George-Hyslop P.H.;
RT "Cloning of a gene bearing missense mutations in early-onset familial
RT Alzheimer's disease."
RL Nature 375:754-760(1995).
RN [3]
RP SEQUENCE FROM N.A.
RA Rowen L., Madan A., Qin S., Abbasi N., Dors M., Dickhoff R., James R.,
RA Loretz C., Lasky S., Madan A., Prescott S., Ratcliffe A., Shaffer T.,
RA Hood L.;
RT "Sequencing of human chromosome 14."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP VARIANTS VNM GLY-213; ARG-273; ASP-316 AND VAL-329.
RX MEDLINE=21583742; PubMed=11704758;
RA Leegwater P.A.J., Vermeulen G., Koenst A.A.M., Naidu S., Mulders J.,
RA Visser A., Kersbergen P., Mobach D., Fonds D., van Berkel C.G.M.,
RA Lemmers R.J.L.F., Frants R.R., Oudejans C.B.M., Schutgens R.B.H.,
RA Pronk J.C., van der Knapp M.S.;
RT "Subunits of the translation initiation factor eIF2B are mutant in
RT leukoencephalopathy with vanishing white matter."
RL Nat. Genet. 29:383-388(2001).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF EUKARYOTIC INITIATION FACTOR

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CC 2-BOUND GDP FOR GTP.
CC -1- SUBUNIT: COMPLEX OF FIVE DIFFERENT SUBUNITS; ALPHA, BETA, GAMMA,
CC DELTA AND EPSILON.
CC -1- DISEASE: Defects in EIF2B2 are a cause of leukoencephalopathy with
CC vanishing white matter (VWM), a brain disease that occurs mainly
CC in children. The neurological signs of VWM include progressive
CC cerebellar ataxia, spasticity, inconsistent optic atrophy and
CC relatively preserved mental abilities. The disease is chronic-
CC progressive with, in most individuals, additional episodes of
CC rapid deterioration following febrile infections or minor head
CC trauma. Head trauma leads only to motor deterioration, whereas
CC infections with fever may end in coma. Death occurs after a
CC variable period of a few years to a few decades, usually following
CC an episode of fever and coma.
CC -1- SIMILARITY: BELONGS TO THE EIF-2B ALPHA/BETA/DELTA SUBUNITS
CC FAMILY.
CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO
CC FRAMESHIFTS.
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CC -----
DR EMBL: AF035280; AAB88176.1; -.
DR EMBL: LA0395; AAC42002.1; ALT_FRAME.
DR EMBL: AC006530; AAD30183.1; -.
DR Genew: HGNC:3258; EIF2B2.
DR MIM: 606454; -.
DR InterPro: IPR000649; IF-2B.
DR Pfam: PF01008; IF-2B; 1.
KW Initiation factor; Protein biosynthesis; Disease mutation.
DR VARIANT 213 213
FT E-> G (IN VWM).
FT /FTid=VAR_012289.
FT VARIANT 273 273
FT K-> R (IN VWM).
FT /FTid=VAR_012321.
FT VARIANT 316 316
FT V-> D (IN VWM).
FT /FTid=VAR_012290.
FT VARIANT 329 329
FT G-> V (IN VWM).
FT /FTid=VAR_012322.
FT CONFLICT 6 6
FT A-> K (IN REF. 2).
FT CONFLICT 23 23
FT K-> T (IN REF. 2).
FT CONFLICT 30 30
FT S-> R (IN REF. 2).
FT CONFLICT 35 35
FT A-> V (IN REF. 2).
FT CONFLICT 52 52
FT S-> R (IN REF. 2).
FT CONFLICT 95 101
FT RLHGRSD-> DSMDAT (IN REF. 2).
FT CONFLICT 110 110
FT H-> D (IN REF. 2).
SQ SEQUENCE 351 AA; 38989 MW; C29FE477143F545A CRC64;

Query Match 42.5%; Score 45; DB 1; Length 351;
Best Local Similarity 72.7%; Pred. No. 27;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Oy 9 RGGGPTSSSEQI 19
    |||||
Db 24 RGGGPRSSSEEM 34

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RESULT 15
MEC2_MOUSE
ID MEC2_MOUSE STANDARD; PRT; 484 AA.
AC 0922D6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Methyl-Cpg-binding protein 2 (Mecp2 protein) (Mecp2).
GN MECP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRATIN=C57BL/6;
RX MEDLINE=98449942; PubMed=9774669;
RA Hendrich B., Bird A.;
RT "Identification and characterization of a family of mammalian methyl-
RT Cpg binding proteins.";
RL Mol. Cell. Biol. 18:6538-6547(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99299240; PubMed=10369871;
RA Coy J.F., Sedlacek Z., Baechner D., Delius H., Poustka A.;
RT "A complex pattern of evolutionary conservation and alternative
RT polyadenylation within the long 3'-untranslated region of the methyl-
RT Cpg-binding protein 2 gene (Mecp2) suggests a regulatory role in gene
RT expression.";
RL Hum. Mol. Genet. 8:1253-1262(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Reichwald K., Thiesen J., Wiehe T., Kioschis P., Straetling W.H.,
RA Rosenthal A., Platzer M.;
RT "Comparative analysis of the methyl Cpg binding protein 2 locus in man
RT and mouse reveals new untranslated sequences.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CHROMOSOMAL PROTEIN THAT BINDS TO METHYLATED DNA. IT CAN
CC BIND SPECIFICALLY TO A SINGLE METHYL-CPG PAIR. IT IS NOT
CC INFLUENCED BY SEQUENCES FLANKING THE METHYL-CPG. MEDIATES
CC TRANSCRIPTIONAL REPRESSION THROUGH INTERACTION WITH HISTONE
CC DEACETYLASE AND THE COREPRESSOR SIN3A (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR. COLOCALIZED WITH METHYL-CPG IN THE
CC GENOME.
CC -1- SIMILARITY: CONTAINS 1 A.T HOOK DNA-BINDING REPEAT.
CC -1- SIMILARITY: CONTAINS 1 METHYL-BINDING DOMAIN (MBD).
CC -----
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CC -----
DR EMBL: AF072251; AAC68880.1; -.
DR EMBL: AJ132922; CAB46495.1; -.
DR EMBL: AF121351; AAF22116.1; -.
DR EMBL: AF158181; AAF33024.1; -.
DR MGD: MGI:99918; Mecp2.
DR InterPro: IPR000637; AT_hook.
DR Pfam: PF01429; MBD; 1.
DR PRINTS: PR00929; ATHOOK.
DR SMART: SM00391; MBD; 1.
KW Transcription regulation; Repressor; DNA-binding; Nuclear protein.
FT DOMAIN 96 149
FT MBD.
FT DOMAIN 277 283
FT POLY-ALA.
FT DOMAIN 366 372
FT POLY-HIS.
FT DOMAIN 384 391
FT POLY-PRO.
FT DOMAIN 440 443
FT POLY-THR.
SQ SEQUENCE 484 AA; 52307 MW; 62FD228F0118A49F CRC64;

Query Match 42.0%; Score 44.5; DB 1; Length 484;
Best Local Similarity 55.6%; Pred. No. 43;
Matches 10; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

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Oy 3 GSGEQPRGGPTSSSEQI 20
    |||
Db 232 GKGE---GGGATTSAGVMA 246

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Search completed: January 7, 2003, 12:29:51
Job time : 8.69231 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:28:08 : Search time 13.8462 Seconds
(without alignments)
138.861 Million cell updates/sec

Title: US-09-876-204-3

Perfect score: 106

Sequence: 1 MDGSGEQPRGCGPTSSFOIM 20

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	143	2	I38921
2	106	100.0	179	2	JC7255
3	106	100.0	192	2	A47538
4	106	100.0	218	2	B47538
5	83	78.3	192	2	D47538
6	65	61.3	41	2	C47538
7	54	50.9	302	2	S71334
8	50	47.2	743	2	T47849
9	49	46.2	513	2	D98225
10	49	46.2	513	2	AC3061
11	49	46.2	1191	2	T13850
12	48	45.3	137	2	G72666
13	47.5	44.8	531	2	T08760
14	47	44.3	397	2	T12436
15	46.5	43.9	321	1	S27501
16	46	43.4	482	1	ERAD24
17	46	43.4	524	2	A69081
18	46	43.4	627	2	T18772
19	46	43.4	654	2	S27004
20	45.5	42.9	434	2	E70111
21	45	42.5	397	2	T30168
22	45	42.5	672	2	T13168
23	45	42.5	1284	2	T13168
24	44.5	42.0	492	2	A41907
25	44.5	42.0	1018	2	T23318
26	44	41.5	247	2	H87703
27	44	41.5	276	1	FIQJ2C
28	44	41.5	352	2	T06463
29	44	41.5	402	2	S02099

30	44	41.5	404	2	S16585	phosphoribulokinas
31	44	41.5	404	2	S15743	phosphoribulokinas
32	44	41.5	571	2	S52276	translational initia
33	44	41.5	642	2	E87332	cobalam biosynth
34	44	41.5	704	2	T34034	hypothetical prote
35	44	41.5	1217	2	T00270	hypothetical prote
36	44	41.5	1241	2	S01827	period clock prote
37	44	41.5	1851	2	T13980	calcium channel al
38	43	40.6	172	2	F84383	hypothetical prote
39	43	40.6	227	2	C90899	probable tail asse
40	43	40.6	335	2	B86429	F26G16.5 protein -
41	43	40.6	340	2	A24026	erythromycin resis
42	43	40.6	382	2	T34789	hypothetical prote
43	43	40.6	476	2	S57963	methyl Cpg binding
44	43	40.6	495	2	T52515	related to n-alkan
45	43	40.6	501	2	G02468	HGIRK1/Kir3.1 - hu

ALIGNMENTS

RESULT 1
I38921
bcl-2-associated protein x, delta splice form - human
N:Alternate names: BAX; programmed cell death membrane protein x delta
C:Species: Homo sapiens (man)
C>Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 17-Nov-2000
C:Accession: I38921
R:Appte, S.S.; Mattei, M.G.; Olsen, B.R.
Genomics 26, 592-594, 1995
A>Title: Mapping of the human BAX gene to chromosome 19q13.3-q13.4 and isolation of a
A:Reference number: I38921; MIM:95331797; PMID:7607685
A:Accession: I38921
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-143 <RES>
A:Cross-references: EMBL:U09599; NID:g841237; PIDN:AMC50142.1; PID:g841238
C:Genetics:
A:Gene: GDB:BAX
A:Cross-references: GDB:228082; OMIM:600040
A:Map position: 19q13.3-19q13.4
C:Superfamily: bcl transforming protein

Query Match 100.0%; Score 106; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGCGPTSSFOIM 20
Db 1 MDGSGEQPRGCGPTSSFOIM 20

RESULT 2
JC7255
Bax-delta protein - human
C:Species: Homo sapiens (man)
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 17-Nov-2000
C:Accession: JC7255
R:Schmitt, E.; Paquet, C.; Beauchemin, M.; Dever-Bertrand, J.; Bertrand, R.
Biochem. Biophys. Res. Commun. 270, 868-879, 2000
A>Title: Characterization of Bax-delta, a cell death-inducing isoform of Bax.
A:Reference number: JC7255
A:Accession: JC7255
A:Molecule type: mRNA
A:Residues: 1-179 <SCH>
A:Cross-references: GB:AF247393
A:Experimental source: cancer promyelocytic cells
C:Comment: This protein, a member of the Bcl-2 family, has a proapoptotic effect. It
C:Superfamily: bcl transforming protein
C:Keywords: transmembrane protein

Query Match 100.0%; Score 106; DB 2; Length 179;

Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSQIM 20
|||||
Db 1 MDGSGEQPRGGGPTSSQIM 20

RESULT 3

A47538

bcl-2-associated protein x, alpha splice form - human

N:Alternate names: BAX; programmed cell death membrane protein x alpha

C:Species: Homo sapiens (man)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000

C:Accession: A47538

R:Oltvai, Z.N.; Millman, C.L.; Korsmeyer, S.J.

Cell 74, 609-619, 1993

A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates

A:Reference number: A47538; MUID:93364978; PMID:8358790

A:Accession: A47538

A:Molecule type: mRNA

A:Residues: 1-192 <OLT>

A:Cross-references: GB:L22473; NID:q388165; PIDN:AAA03619.1; PID:q388166

A:Note: the amino end of the mature protein is blocked

C:Genetics:

A:Gene: GDB:BAX

A:Cross-references: GDB:228082; OMIM:600040

A:Map position: 19q13.3-19q13.4

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; blocked amino end; heterodimer; homodimer; transmembrane

F:172-191/Domain: transmembrane status predicted <TM1>

Query Match 100.0%; Score 106; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 4.4e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSQIM 20
|||||
Db 1 MDGSGEQPRGGGPTSSQIM 20

RESULT 4

B47538

bcl-2-associated protein x, beta splice form - human

N:Alternate names: BAX; programmed cell death membrane protein x beta

C:Species: Homo sapiens (man)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000

C:Accession: B47538

R:Oltvai, Z.N.; Millman, C.L.; Korsmeyer, S.J.

Cell 74, 609-619, 1993

A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates

A:Reference number: A47538; MUID:93364978; PMID:8358790

A:Accession: B47538

A:Molecule type: mRNA

A:Residues: 1-218 <OLT>

A:Cross-references: GB:L22474; NID:q388167; PIDN:AAA03620.1; PID:q388168

A:Note: the amino end of the mature protein is blocked

C:Genetics:

A:Gene: GDB:BAX

A:Cross-references: GDB:228082; OMIM:600040

A:Map position: 19q13.3-19q13.4

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; blocked amino end; cytosol; heterodimer; homodimer

Query Match 100.0%; Score 106; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSQIM 20
|||||
Db 1 MDGSGEQPRGGGPTSSQIM 20

RESULT 5
D47538
bcl-2-associated protein x - mouse

N:Alternate names: BAX; programmed cell death membrane protein x

C:Species: Mus musculus (house mouse)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000

C:Accession: D47538

R:Oltvai, Z.N.; Millman, C.L.; Korsmeyer, S.J.

Cell 74, 609-619, 1993

A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerate

A:Reference number: A47538; MUID:93364978; PMID:8358790

A:Accession: D47538

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-192 <OLT>

A:Cross-references: GB:L22472

C:Genetics:

A:Gene: bax

C:Superfamily: bcl transforming protein

Query Match 78.3%; Score 83; DB 2; Length 192;
Best Local Similarity 85.0%; Pred. No. 9.1e-05;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSQIM 20
|||||
Db 1 MDGSGEQPRGGGPTSSQIM 20

RESULT 6

C47538

bcl-2-associated protein x, gamma splice form - human

N:Alternate names: BAX; programmed cell death membrane protein x gamma

C:Species: Homo sapiens (man)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Oct-1999

C:Accession: C47538

R:Oltvai, Z.N.; Millman, C.L.; Korsmeyer, S.J.

Cell 74, 609-619, 1993

A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerate

A:Reference number: A47538; MUID:93364978; PMID:8358790

A:Accession: C47538

A:Molecule type: mRNA

A:Residues: 1-41 <OLT>

A:Cross-references: GB:L22475; NID:q388169; PIDN:AAA03621.1; PID:q388170

A:Note: the amino end of the mature protein is blocked

C:Genetics:

A:Gene: GDB:BAX

A:Cross-references: GDB:228082; OMIM:600040

A:Map position: 19q13.3-19q13.4

C:Keywords: alternative splicing; blocked amino end; cytosol; heterodimer; homodimer

Query Match 61.3%; Score 65; DB 2; Length 41;
Best Local Similarity 72.2%; Pred. No. 0.0074;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSQIM 18
|||||
Db 1 MDGSGEQPRGGGPTSSQIM 18

RESULT 7

S71334

acetyl xylan esterase precursor - fungus (Trichoderma reesei)

C:Species: Trichoderma reesei

C>Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 17-Mar-1999

C:Accession: S71334

R:Margolis-Clark, E.; Tenkanen, M.; Soederlund, H.; Penttilae, M.

Eur. J. Biochem. 237, 553-560, 1996

A:Title: Acetyl xylan esterase from Trichoderma reesei contains an active-site serine

A:Reference number: S71334; MUID:96235218; PMID:8647098

A:Accession: S71334

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-302 <MAR>
A:Cross-References: EMBL:D69256; NID:g1431619; PID:e220701; PID:g1431620
C:Genetics:
A:Gene: axel
C:Superfamily: fungal cellulose-binding domain homology
F:1-20/Domains: signal sequence #status predicted <SIG>
F:21-302/Product: acetyl xylan esterase #status predicted <MAT>
F:271-302/Domains: fungal cellulose-binding domain homology <FCB>

Query Match 50.9%; Score 54; DB 2; Length 302;
Best Local Similarity 50.0%; Pred. No. 2.2;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 1 MDGSGQPRGGGPTSSQ 18
DB 237 LSSGSGQPRGGGPTSSR 254

RESULT 8
T47849
hypothetical protein T8B10.40 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T47849
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, submitted to the Protein Sequence Database, March 2000
A:Reference number: 224478
A:Accession: T47849
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-743 <RIE>
A:Cross-References: EMBL:AL138646
A:Experimental source: cultivar Columbia; BAC clone T8B10
C:Genetics:
A:Map position: 3
A:Note: T8B10.40

Query Match 47.2%; Score 50; DB 2; Length 743;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SGEQPRGG 12
DB 725 SGEQPRGG 733

RESULT 9
D98225
hypothetical protein AGR_L1495 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C:Accession: D98225
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2333-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; PMID:11743194
A:Accession: D98225
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-513 <KUR>
A:Cross-References: GB:AE007870; PIDN:AAK89326.1; PID:g15159166; GSPDB:GN00170
C:Genetics:
A:Gene: AGR_L1495
A:Map position: linear chromosome

Query Match 46.2%; Score 49; DB 2; Length 513;
Best Local Similarity 56.2%; Pred. No. 20;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 3 GSGEQPRGGGPTSSQ 18
DB 444 GSETPPRGGGPFSDE 459

RESULT 10
AC3061
hypothetical protein ACU4105 [imported] - Agrobacterium tumefaciens (strain C58, Dupc
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AC3061
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moe
erage, G.; Giller, W.; Grant, C.; Guentner, D.; Kuyavin, T.; Levy, R.; Li, M.; McCle
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AC3061
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-513 <KUR>
A:Cross-References: GB:AE008689; PIDN:AAU44905.1; PID:g17742557; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: ACU4105
A:Map position: linear chromosome

Query Match 46.2%; Score 49; DB 2; Length 513;
Best Local Similarity 56.2%; Pred. No. 20;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 3 GSGEQPRGGGPTSSQ 18
DB 444 GSETPPRGGGPFSDE 459

RESULT 11
T13850
gene u-shaped protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13850
R:Haenlin, M.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z17795
A:Accession: T13850
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1191 <HAE>
A:Cross-References: EMBL:Y12322; NID:e1169964; PID:e1169965; PIDN:CAA72991.1
C:Genetics:
A:Gene: u-shaped
A:Cross-References: FlyBase:FBgn0003963
C:Function:
A:Description: acts as a transregulator of achete and scute in the dorsal region of
C:Keywords: zinc finger

Query Match 46.2%; Score 49; DB 2; Length 1191;
Best Local Similarity 50.0%; Pred. No. 46;
Matches 11; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

OY 3 GSG----EOPRGGPTSSQIM 20
DB 578 GTEKENVETPRGGGVTPEQIV 599

RESULT 12
G72666
hypothetical protein ABE0758 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C:Accession: G72666
R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.

DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
A:Reference number: A72450; MUID:9310339; PMID:10382966
A:Accession: G72666
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-137 <RAW>
A:Cross-references: DDBJ:AP000060; NID:g5104188; PID:BA079735.1; PID:Q1043521; PID:g510
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE0758
C:Superfamily: Aeropyrum pernix hypothetical protein APE0758

Query Match 45.3%; Score 48; DB 2; Length 137;
Best Local Similarity 66.7%; Pred. No. 7.1;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 DSGEQPRGGGPTSS 16
||| ||||| |||
Db 80 DGLHSPRGCGSGSS 94

RESULT 13
T08760
hypothetical protein DKFZP586M1019.1 - human
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C:Accession: T08760
R:Wambolt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z16471
A:Accession: T08760
A:Molecule type: mRNA
A:Residues: 1-531 <RAW>
A:Cross-references: EMBL:AL050284
A:Experimental source: adult uterus; clone DKFZP586M1019
C:Genetics:
A:Note: DKFZP586M1019.1

Query Match 44.8%; Score 47.5; DB 2; Length 531;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

OY 2 DGS-GEQPRGGG 12
||| ||||| |||
Db 113 EGSPGEQPRGGG 124

RESULT 14
T12436
phosphoribulokinase (EC 2.7.1.19) - common ice plant
C:Species: Mesembryanthemum crystallinum (common ice plant)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 20-Sep-1999
C:Accession: T12436
R:Michalowski, C.B.; DeRocher, E.J.; Bohner, H.J.; Salvucci, M.E.
submitted to the EMBL Data Library, July 1991
A:Description: Phosphoribulokinase from ice plant; transcription, transcripts and prote
A:Reference number: Z17516
A:Accession: T12436
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-397 <MIC>
A:Cross-references: EMBL:M73707; NID:g167265; PID:g167266
C:Superfamily: phosphoribulokinase
C:Keywords: ATP; Calvin cycle; phosphotransferase

Query Match 44.3%; Score 47; DB 2; Length 397;
Best Local Similarity 52.9%; Pred. No. 29;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 3 GSGEQPRGGGPTSSQI 19
||| ||||| |||
Db 77 GAAPPRGGNDPSNTLI 93

RESULT 15
S27501
alkaline proteinase (EC 3.4.21.-), intracellular - Bacillus sp. (strain 221)
C:Species: Bacillus sp.
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: S27501
R:Kato, C.; Nakano, Y.; Yamamoto, M.; Horikoshi, K.
submitted to the EMBL Data Library, March 1992
A:Description: Cloning and nucleotide sequence of the intracellular alkaline protease
A:Reference number: S27501
A:Accession: S27501
A:Molecule type: DNA
A:Residues: 1-321 <RAW>
A:Cross-references: EMBL:D10730; NID:g216233; PID:BA01573.1; PID:g216234
C:Superfamily: Bacillus intracellular serine proteinase; subtilisin homology
C:Keywords: hydrolase; serine proteinase
F:40-264/Domain: subtilisin homology <SPR>
F:49,86,250/Active site: Asp, His, Ser #status predicted

Query Match 43.9%; Score 46.5; DB 1; Length 321;
Best Local Similarity 30.2%; Pred. No. 28;
Matches 13; Conservative 3; Mismatches 2; Indels 25; Gaps 2;

OY 2 DSGEQ-----PRG-----CGPTSSQI 19
||| ||| ||| ||| |||
Db 121 DSGEMGWIKAIRYAVDWRGPKGEQMRITMSLGGPTDSDEL 163

Search completed: January 7, 2003, 12:31:22
Job time : 15.8462 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:28:23 : Search time 11.7949 Seconds
(without alignments)
49.891 Million cell updates/sec

Title: US-09-876-204-3
Perfect score: 106
Sequence: 1 MDGSGEQPRGGGPTSSSEQIM 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents-AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCtUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	20	4	US-09-166-028-3
2	106	100.0	192	1	US-08-112-208C-2
3	106	100.0	192	1	US-08-112-208C-9
4	106	100.0	192	1	US-08-248-819A-2
5	106	100.0	192	1	US-08-248-819A-9
6	106	100.0	192	1	US-08-607-269-25
7	106	100.0	192	1	US-08-471-058-13
8	106	100.0	192	2	US-08-337-646A-2
9	106	100.0	192	2	US-08-337-646A-9
10	106	100.0	192	2	US-08-856-531-2
11	106	100.0	192	2	US-08-856-531-9
12	106	100.0	192	2	US-08-856-034-2
13	106	100.0	192	2	US-08-856-034-9
14	106	100.0	192	3	US-08-471-057-13
15	106	100.0	192	4	US-09-127-048-7
16	106	100.0	192	4	US-08-927-326-2
17	106	100.0	192	4	US-08-927-326-9
18	106	100.0	192	5	PCT-US93-04600-25
19	106	100.0	221	1	US-08-616-732A-9
20	106	100.0	221	4	US-09-037-742B-9
21	83	78.3	192	4	US-09-166-028-4
22	83	78.3	192	1	US-08-112-208C-3
23	83	78.3	192	1	US-08-112-208C-8
24	83	78.3	192	1	US-08-248-819A-3
25	83	78.3	192	1	US-08-248-819A-8
26	83	78.3	192	2	US-08-337-646A-3
27	83	78.3	192	2	US-08-337-646A-8

28	83	78.3	192	2	US-08-856-531-3	Sequence 3, Appl1
29	83	78.3	192	2	US-08-856-531-8	Sequence 8, Appl1
30	83	78.3	192	2	US-08-856-034-3	Sequence 3, Appl1
31	83	78.3	192	2	US-08-856-034-8	Sequence 8, Appl1
32	83	78.3	192	4	US-09-127-048-6	Sequence 6, Appl1
33	83	78.3	192	4	US-08-927-326-3	Sequence 3, Appl1
34	83	78.3	192	4	US-08-927-326-8	Sequence 8, Appl1
35	81	76.4	20	4	US-09-166-028-5	Sequence 5, Appl1
36	79	74.5	25	1	US-08-798-897-21	Sequence 21, Appl1
37	79	74.5	25	2	US-08-978-523-21	Sequence 21, Appl1
38	67	63.2	19	4	US-09-166-028-1	Sequence 1, Appl1
39	65	61.3	41	1	US-08-112-208C-7	Sequence 7, Appl1
40	65	61.3	41	1	US-08-248-819A-7	Sequence 7, Appl1
41	65	61.3	41	2	US-08-337-646A-7	Sequence 7, Appl1
42	65	61.3	41	2	US-08-856-531-7	Sequence 7, Appl1
43	65	61.3	41	2	US-08-856-034-7	Sequence 7, Appl1
44	65	61.3	41	4	US-08-927-326-7	Sequence 7, Appl1
45	45	42.5	1284	4	US-09-343-494-9	Sequence 9, Appl1

ALIGNMENTS

```
RESULT 1
US-09-166-028-3
; Sequence 3, Application US/09166028
; Patent No. 6245885
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/166,028
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-028-3

Query Match      100.0%; Score 106; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDGSGEQPRGGGPTSSSEQIM 20
DB      1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 2
US-08-112-208C-2
; Sequence 2, Application US/08112208C
; Patent No. 5691179
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/112,208C
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FILING DATE: 26-AUG-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SMITH, WILLIAM M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-112-208C-2

Query Match 100.0%; Score 106; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDSSGEQPRGGGPTSSSEQIM 20
Db 1 MDSSGEQPRGGGPTSSSEQIM 20

RESULT 3
US-08-112-208C-9
Sequence 9, Application US/08112208C
Patent No. 5691179
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourlie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/112,208C
FILING DATE: 26-AUG-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-112-208C-9

Query Match 100.0%; Score 106; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDSSGEQPRGGGPTSSSEQIM 20
Db 1 MDSSGEQPRGGGPTSSSEQIM 20

RESULT 4
US-08-248-819A-2
Sequence 2, Application US/08248819A
Patent No. 5700638
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourlie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,819A
FILING DATE: 25-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-248-819A-2

Query Match 100.0%; Score 106; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDSSGEQPRGGGPTSSSEQIM 20
Db 1 MDSSGEQPRGGGPTSSSEQIM 20

RESULT 5
US-08-248-819A-9
Sequence 9, Application US/08248819A
Patent No. 5700638
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourlie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,819A
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-248-819A-9
;
Query Match 100.0%; Score 106; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1,8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEQPRGGGPTSSSEQIM 20
Db 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 6
US-08-607-269-25
; Sequence 25, Application US/08607269
; Patent No. 5702897
; GENERAL INFORMATION:
; APPLICANT: Reed, John C
; TITLE OF INVENTION: Interaction of Proteins Involved in a
; TITLE OF INVENTION: Cell Death Pathway
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 Le Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/607,269
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/226,876
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;

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US-08-607-269-25
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Query Match 100.0%; Score 106; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1,8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEQPRGGGPTSSSEQIM 20
Db 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 7
US-08-471-058-13
; Sequence 13, Application US/08471058
; Patent No. 5770443
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Barr, Philip J.
; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
; TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,058
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; APPLICATION NUMBER: 08/160,067
; FILING DATE: 30-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lennhardt, Susan K
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-471-058-13
;
Query Match 100.0%; Score 106; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1,8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEQPRGGGPTSSSEQIM 20
Db 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 8
US-08-337-646A-2
; Sequence 2, Application US/08337646A
; Patent No. 5856171
; GENERAL INFORMATION:
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APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Hourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,646A
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-337-646A-2

Query Match 100.0%; Score 106; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1,8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGGPTSSSEQIM 20
Db 1 MDGSGEOPRGGPTSSSEQIM 20

RESULT 9
US-08-337-646A-9
Sequence 9, Application US/08337646A
Patent No. 5856171
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Hourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,646A
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-337-646A-9

Query Match 100.0%; Score 106; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1,8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGGPTSSSEQIM 20
Db 1 MDGSGEOPRGGPTSSSEQIM 20

RESULT 10
US-08-856-531-2
Sequence 2, Application US/08856531
Patent No. 5942490
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,531
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, Donald R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..192
OTHER INFORMATION: /note= "Human BAX polypeptide"

US-08-856-531-2

Query Match

Best Local Similarity 100.0%; Score 106; DB 2; Length 192;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGCPTSSSEQIM 20

Db 1 MDGSGEQPRGGCPTSSSEQIM 20

RESULT 11

US-08-856-531-9
Sequence 9, Application US/08856531
Patent No. 5942490

GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.

TITLE OF INVENTION: CELL DEATH REGULATORS

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howell & Haferkamp, L.C.

STREET: 7733 Forsyth Blvd., Suite 1400

CITY: St. Louis

STATE: MO

COUNTRY: USA

ZIP: 63105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/856,531

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, Donald R.

REGISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 976176

TELECOMMUNICATION INFORMATION:

TELEPHONE: 314-727-6092

TELEFAX: 314-727-5188

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..192

OTHER INFORMATION: /note="Human BAX polypeptide"

US-08-856-531-9

QY 1 MDGSGEQPRGGCPTSSSEQIM 20

Db 1 MDGSGEQPRGGCPTSSSEQIM 20

RESULT 12

US-08-856-034-2
Sequence 2, Application US/08856034
Patent No. 5955595

GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.

TITLE OF INVENTION: CELL DEATH REGULATORS

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howell & Haferkamp, L.C.

STREET: 7733 Forsyth Blvd., Suite 1400

CITY: St. Louis

STATE: MO

COUNTRY: USA

ZIP: 63105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/856,034

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, Donald R.

REGISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 976175

TELECOMMUNICATION INFORMATION:

TELEPHONE: 314-727-6092

TELEFAX: 314-727-5188

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 192 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Protein

LOCATION: 1..192

OTHER INFORMATION: /note="Human BAX polypeptide"

US-08-856-034-2

QY 1 MDGSGEQPRGGCPTSSSEQIM 20

Db 1 MDGSGEQPRGGCPTSSSEQIM 20

RESULT 13

US-08-856-034-9
Sequence 9, Application US/08856034
Patent No. 5955595

GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.

TITLE OF INVENTION: CELL DEATH REGULATORS

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howell & Haferkamp, L.C.

STREET: 7733 Forsyth Blvd., Suite 1400

CITY: St. Louis

STATE: MO

COUNTRY: USA

ZIP: 63105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/856,034

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, Donald R.

REGISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 976175

TELECOMMUNICATION INFORMATION:

TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: protein
LOCATION: 1..192
OTHER INFORMATION: /note="Human BAX polypeptide"
US-08-856-034-9

Query Match 100.0%; Score 106; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSSEQIM 20
DB 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 14
US-08-471-057-13
Sequence 13, Application US/08471057
Patent No. 6015687
GENERAL INFORMATION:
APPLICANT: KIEPER, MICHAEL C.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,057
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-057-13

Query Match 100.0%; Score 106; DB 3; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSSEQIM 20
DB 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 15
US-09-127-048-7
Sequence 7, Application US/09127048
Patent No. 6165732
GENERAL INFORMATION:
APPLICANT: Korsmeyer, Stanley J.
APPLICANT: Schlessinger, Paul H.
TITLE OF INVENTION: Method for Identifying Apoptosis Modulating Compounds
FILE REFERENCE: 6029-6052
CURRENT APPLICATION NUMBER: US/09/127,048
CURRENT FILING DATE: 1998-07-31
EARLIER APPLICATION NUMBER: 60/061,823
EARLIER FILING DATE: 1997-10-14
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
US-09-127-048-7

Query Match 100.0%; Score 106; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.8e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSSEQIM 20
DB 1 MDGSGEQPRGGGPTSSSEQIM 20

Search completed: January 7, 2003, 12:31:49
Job time: 11.7949 secs

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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:31:28 : Search time 30.2051 Seconds
(without alignments)
83.819 Million cell updates/sec

Title: US-09-876-204-1

Perfect score: 19
Sequence: 1 MDGSGXXXXGGPTSSQI 19

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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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- 14: /SIDS2/gcgcdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDS2/gcgcdata/geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDS2/gcgcdata/geneseq/geneseq-emb1/AA1995.DAT:*
- 17: /SIDS2/gcgcdata/geneseq/geneseq-emb1/AA1996.DAT:*
- 18: /SIDS2/gcgcdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDS2/gcgcdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDS2/gcgcdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDS2/gcgcdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDS2/gcgcdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgcdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	14	73.7	19	21	AAV90735	Apoptotic regulati
2	9	47.4	20	21	AAV90736	Human BAX amino ac
3	9	47.4	20	21	AAV90737	Mouse BAX amino ac
4	9	47.4	20	21	AAV90738	Rat BAX amino acid
5	9	47.4	70	21	AAV70816	Human neuroprotect
6	9	47.4	70	21	AAV70817	Mouse neuroprotect
7	9	47.4	70	21	AAV70820	Human neuroprotect
8	9	47.4	70	21	AAV70821	Mouse neuroprotect
9	9	47.4	78	21	AAV70818	Human neuroprotect
10	9	47.4	78	21	AAV70819	Mouse neuroprotect

11	9	47.4	78	21	AAV70822	Human neuroprotect
12	9	47.4	78	21	AAV70823	Mouse neuroprotect
13	9	47.4	131	20	AAV34149	Human truncated Ba
14	9	47.4	192	16	AAV71406	Human Bax protein.
15	9	47.4	192	16	AAV71407	Murine Bax protein
16	9	47.4	192	20	AAV34150	Human wild-type Ba
17	9	47.4	192	20	AAV05434	Mouse BAX protein
18	9	47.4	192	20	AAV05435	Human BAX protein
19	9	47.4	192	20	AAV87804	A human Bcl-2 asso
20	9	47.4	192	20	AAV87805	Murine Bcl-2 assoc
21	9	47.4	192	20	AAV87808	Murine Bcl-2 assoc
22	9	47.4	192	21	AAV87809	A human Bcl-2 asso
23	9	47.4	192	21	AAV70827	Human BAX alpha pr
24	9	47.4	192	21	AAV70828	Mouse BAX alpha pr
25	9	47.4	192	21	AAV69202	Amino acid sequenc
26	9	47.4	192	22	AAV74121	Human bcl-2 associ
27	9	47.4	192	22	AAV74122	Murine bcl-2 assoc
28	9	47.4	192	22	AAV74125	Murine bcl-2 assoc
29	9	47.4	192	22	AAV74126	Human bcl-2 associ
30	9	47.4	192	22	AAV848286	Human Bax protein.
31	9	47.4	192	22	AAV835128	Murine Bax. Mus s
32	9	47.4	192	22	AAV835129	Human Bax. Homo s
33	9	47.4	192	22	AAV850539	Human Bax protein
34	9	47.4	192	23	AAV76551	Murine Bax polypep
35	9	47.4	192	23	AAV76552	Human Bax polypept
36	9	47.4	197	21	AAV78512	Truncated Bax amin
37	9	47.4	221	18	AAV10688	Bax omega protein,
38	9	47.4	331	20	AAV39263	Coding region of c
39	6	31.6	94	22	AAV49519	Staphylococcus epi
40	6	31.6	120	23	ABP40487	Arabidopsis thalia
41	6	31.6	130	21	AAV34513	Arabidopsis thalia
42	6	31.6	141	21	AAV34512	Arabidopsis thalia
43	6	31.6	148	21	AAV34511	Arabidopsis thalia
44	6	31.6	253	22	AAV63461	Human breast cance
45	6	31.6	267	22	AAV14611	Novel bone marrow

ALIGNMENTS

RESULT 1
ID AAV90735 standard: peptide: 19 AA.
XX AAV90735:
AC
XX 17-AUG-2000 (first entry)
DT
XX
DE Apoptotic regulation of targeting domain consensus sequence SPQ ID NO:1.
XX
KW Apoptotic regulation of targeting domain; ART domain; BAX; apoptosis;
KW cell death; cancer; cytostatic.
XX
XX Homo sapiens.
OS Mus musculus.
OS Rattus norvegicus.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 6 /label= Glu, Asp
FT Misc-difference 7 /label= Gln, His
FT Misc-difference 8 /label= Leu, Pro
FT Misc-difference 9 /label= Arg, Gly
FT Misc-difference 10 /label= Ser, Gly
XX
XX WO200020446-A2.
XX 13-APR-2000.

PF 05-OCT-1999; 99WO-IB01680.
XX
PR 05-OCT-1998; 98US-0166028.
XX
XX (UYMC-) UNIV MCGILL.
XX
PI Shore GC, Gopling S;
XX
DR WPI; 2000-303740/26.
XX
PT BAX polypeptide lacking an ART domain, useful for identifying agents
XX that modulate apoptosis which can then be used for treating cancer -
XX
PS Disclosure; Page 6; 53pp; English.
XX
CC The present invention describes a pure protein (P1) comprising a BAX
CC polypeptide lacking an apoptotic regulation of targeting (ART) domain.
CC P1 has cytostatic activity and can be used in the modulation of
CC apoptosis. The polypeptides and methods from the present invention are
CC useful for identifying compounds that modulate apoptosis which can then
CC be used for treating cancer. The present sequence represents a consensus
CC sequence for an ART domain derived from human, mouse and rat, which is
CC given in the exemplification of the present invention.
XX
SQ Sequence 19 AA:

Query Match 73.7%; Score 14; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGXXXXXGGPSSSEQI 19
|||
Db 1 MDGSGXXXXXGGPSSSEQI 19

RESULT 2
AAV90736
ID AAV90736 standard; peptide: 20 AA.
XX
AC AAV90736;
XX
DT 17-AUG-2000 (first entry)
XX
DE Human BAX amino acid sequence 1 to 20 SEQ ID NO:2.
XX
KM Apoptotic regulation of targeting domain; ART domain; BAX; apoptosis;
KM cell death; cancer; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200020446-A2.
XX
PD 13-APR-2000.
XX
PE 05-OCT-1999; 99WO-IB01680.
XX
PR 05-OCT-1998; 98US-0166028.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Shore GC, Gopling S;
XX
DR WPI; 2000-303740/26.
XX
PT BAX polypeptide lacking an ART domain, useful for identifying agents
XX that modulate apoptosis which can then be used for treating cancer -
XX
PS Example 2; Page 52; 53pp; English.
XX
CC The present invention describes a pure protein (P1) comprising a BAX
CC polypeptide lacking an apoptotic regulation of targeting (ART) domain.
CC P1 has cytostatic activity and can be used in the modulation of
CC apoptosis. The polypeptides and methods from the present invention are

CC useful for identifying compounds that modulate apoptosis which can then
CC be used for treating cancer. The present sequence represents a human
CC BAX peptide sequence of amino acids 1 to 20, which is used in an
CC example from the present invention.
XX
SQ Sequence 20 AA:

Query Match 47.4%; Score 9; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSSEQI 19
|||
Db 11 GGPTSSSEQI 19

RESULT 3
AAV90737
ID AAV90737 standard; peptide: 20 AA.
XX
AC AAV90737;
XX
DT 17-AUG-2000 (first entry)
XX
DE Mouse BAX amino acid sequence 1 to 20 SEQ ID NO:3.
XX
KM Apoptotic regulation of targeting domain; ART domain; BAX; apoptosis;
KM cell death; cancer; cytostatic.
XX
OS Mus musculus.
XX
PN WO200020446-A2.
XX
PD 13-APR-2000.
XX
PE 05-OCT-1999; 99WO-IB01680.
XX
PR 05-OCT-1998; 98US-0166028.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Shore GC, Gopling S;
XX
DR WPI; 2000-303740/26.
XX
PT BAX polypeptide lacking an ART domain, useful for identifying agents
XX that modulate apoptosis which can then be used for treating cancer -
XX
PS Example 2; Page 53; 53pp; English.
XX
CC The present invention describes a pure protein (P1) comprising a BAX
CC polypeptide lacking an apoptotic regulation of targeting (ART) domain.
CC P1 has cytostatic activity and can be used in the modulation of
CC apoptosis. The polypeptides and methods from the present invention are
CC useful for identifying compounds that modulate apoptosis which can then
CC be used for treating cancer. The present sequence represents a mouse
CC BAX peptide sequence of amino acids 1 to 20, which is used in an
CC example from the present invention.
XX
SQ Sequence 20 AA:

Query Match 47.4%; Score 9; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSSEQI 19
|||
Db 11 GGPTSSSEQI 19

RESULT 4
AAV90738
ID AAV90738 standard; peptide: 20 AA.

```
XX AC AAY90738:
XX
XX
XX DT 17-AUG-2000 (first entry)
XX
XX DE Rat BAX amino acid sequence 1 to 20 SEQ ID NO:4.
XX
XX DE Apoptotic regulation of targeting domain; ART domain; BAX: apoptosis;
XX cell death; cancer; cytostatic.
XX OS Rattus norvegicus.
XX PN WO200020446-A2.
XX
XX PD 13-APR-2000.
XX
XX PF 05-OCT-1999; 99WO-1B01680.
XX
XX PR 05-OCT-1998; 98US-0166028.
XX
XX PA (UYMC-) UNIV MCGILL.
XX
XX PI Shore GC, Goping S;
XX
XX DR WPI: 2000-303740/26.
XX
XX PT BAX polypeptide lacking an ART domain, useful for identifying agents
XX that modulate apoptosis which can then be used for treating cancer -
XX
XX PS Example 2: Page 53; 53pp; English.
XX
XX CC The present invention describes a pure protein (PI) comprising a BAX
XX polypeptide lacking an apoptotic regulation of targeting (ART) domain.
XX CC PI has cytostatic activity and can be used in the modulation of
XX apoptosis. The polypeptides and methods from the present invention are
XX useful for identifying compounds that modulate apoptosis which can then
XX be used for treating cancer. The present sequence represents a rat
XX CC BAX peptide sequence of amino acids 1 to 20, which is used in an
XX example from the present invention.
XX
XX SQ Sequence 20 AA:
XX
XX Query Match 47.4%; Score 9; DB 21; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 0.027;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 11 GGPTSSEQI 19
XX
XX DB 11 GGPTSSEQI 19
XX
XX RESULT 5
XX AAY70816
XX ID AAY70816 standard; Protein: 70 AA.
XX
XX AC AAY70816;
XX
XX DT 31-JUL-2000 (first entry)
XX
XX DE Human neuroprotective truncated BAX protein, tBAX70.
XX
XX KW Human: truncated BAX protein; tBAX70; BAX alpha; BCL-2 family;
XX neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
XX apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
XX spinal cord injury; head trauma; stroke.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT 1..58
XX FT /note= "N-terminal region of BAX alpha"
XX FT 59..70
XX FT /label= Partial_BH3_domain
```

```
FT FT /note= "BH3 domain in the full-length BAX alpha consists
FT FT of amino acids 59-73"
XX
XX PN WO200023083-A1.
XX
XX PD 27-APR-2000.
XX
XX PF 22-OCT-1999; 99WO-US24747.
XX
XX PR 22-OCT-1998; 98US-0177315.
XX
XX PA (UNIW ) UNIV WASHINGTON.
XX
XX PI Johnson EM, Easton R;
XX
XX DR WPI: 2000-339513/29.
XX
XX PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
XX for the treatment of nervous system disorders -
XX
XX PS Claim 4; Page 32; 43pp; English.
XX
XX CC The present sequence is a specifically claimed truncated BAX protein
XX tBAX70 which inhibits neuronal apoptosis induced by trophic factor
XX CC deprivation. The protein consists of first 70 amino acids of human
XX CC BAX alpha, that includes the N-terminal region and a portion of the BH3
XX CC domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of
XX CC the full-length BAX alpha. The tBAX protein lacking only the
XX CC transmembrane domain has been shown to have anti-apoptotic activity.
XX CC The present sequence is used to treat diseases associated with neuronal
XX CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
XX CC spinal cord injury, head trauma and stroke.
XX
XX SQ Sequence 70 AA:
XX
XX Query Match 47.4%; Score 9; DB 21; Length 70;
XX Best Local Similarity 100.0%; Pred. No. 0.081;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 11 GGPTSSEQI 19
XX
XX DB 11 GGPTSSEQI 19
XX
XX RESULT 6
XX AAY70817
XX ID AAY70817 standard; Protein: 70 AA.
XX
XX AC AAY70817;
XX
XX DT 31-JUL-2000 (first entry)
XX
XX DE Mouse neuroprotective truncated BAX protein, tBAX70.
XX
XX KW Mouse: truncated BAX protein; tBAX70; BAX alpha; BCL-2 family;
XX neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
XX apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
XX spinal cord injury; head trauma; stroke.
XX
XX OS Mus musculus.
XX
XX FH Key Location/Qualifiers
XX FT 1..58
XX FT /note= "N-terminal region of BAX alpha"
XX FT 59..70
XX FT /label= Partial_BH3_domain
XX FT /note= "BH3 domain in the full-length BAX alpha consists
XX FT of amino acids 59-73"
```

PF 22-OCT-1999; 99WO-US24747.
XX
XX 22-OCT-1998; 98US-0177315.
XX
XX (UNIW) UNIV WASHINGTON.
PA
XX Johnson EM, Easton R;
XX WPI; 2000-339513/29.
XX
XX Truncated Bax polypeptides useful for preventing apoptosis of neurons
PT for the treatment of nervous system disorders -
PT
XX Claim 4; Page 32; 43pp; English.
XX
XX The present sequence is a specifically claimed truncated BAX protein
CC tBAX70 which inhibits neuronal apoptosis induced by trophic factor
CC deprivation. The protein consists of first 70 amino acids of mouse
CC BAX alpha, that includes the N-terminal region and a portion of the BH3
CC domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of
CC the full-length BAX alpha. The tBAX protein lacking only the
CC transmembrane domain has been shown to have anti-apoptotic activity.
CC The present sequence is used to treat diseases associated with neuronal
CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
CC spinal cord injury, head trauma and stroke.
XX
XX Sequence 70 AA:
SQ
Query Match 47.4%; Score 9; DB 21; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.081.
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GGPRSSQEI 19
Db 11 GGPRSSQEI 19
RESULT 7
AAV70820
ID AAV70820 standard; Protein; 70 AA.
XX
XX AAV70820;
AC
XX 31-JUL-2000 (first entry)
DT
XX
XX Human neuroprotective truncated BAX protein tBAX70 mutant.
DE
XX
XX Human: truncated BAX protein; tBAX70M; BAX alpha; BCL-2 family; mutant;
KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
KW spinal cord injury; head trauma; stroke.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 1..58
FT /note= "N-terminal region from BAX alpha"
FT Domain 59..70
FT /label= Partial_BH3_domain
FT /note= "BH3 domain in the full-length BAX alpha consists
FT Misc-difference 55
FT of amino acids 59-73"
FT
FT Misc-difference 55
FT /note= "Wild type Ser is substituted by Ala"
FT MISC-difference 60
FT /note= "Wild type Ser is substituted by Ala"
XX
XX WO200023083-A1.
XX
XX 27-APR-2000.
XX
XX 22-OCT-1999; 99WO-US24747.
XX

PR 22-OCT-1998; 98US-0177315.
XX
XX (UNIW) UNIV WASHINGTON.
PA
XX Johnson EM, Easton R;
XX WPI; 2000-339513/29.
XX
XX Truncated Bax polypeptides useful for preventing apoptosis of neurons
PT for the treatment of nervous system disorders -
PT
XX Claim 4; Page 33-34; 43pp; English.
XX
XX The present sequence is a specifically claimed truncated BAX protein,
CC tBAX70 mutant (tBAX70M) which inhibits neuronal apoptosis induced by
CC trophic factor deprivation. The protein consists of the N-terminal
CC region and a portion of BH3 domain of human BAX alpha.
CC It lacks the BH1, BH2 and C-terminal transmembrane
CC domains of the full-length BAX alpha. The tBAX protein lacking only the
CC transmembrane domain has been shown to have anti-apoptotic activity.
CC The present sequence is used to treat diseases associated with neuronal
CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
CC spinal cord injury, head trauma and stroke.
XX
XX Sequence 70 AA:
SQ
Query Match 47.4%; Score 9; DB 21; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.081.
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GGPRSSQEI 19
Db 11 GGPRSSQEI 19
RESULT 8
AAV70821
ID AAV70821 standard; Protein; 70 AA.
XX
XX AAV70821;
AC
XX 31-JUL-2000 (first entry)
DT
XX
XX Mouse neuroprotective truncated BAX protein tBAX70 mutant.
DE
XX
XX Mouse: truncated BAX protein; tBAX70M; BAX alpha; BCL-2 family; mutant;
KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
KW spinal cord injury; head trauma; stroke.
XX
XX Mus musculus.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH 1..58
FT /note= "N-terminal region from BAX alpha"
FT Domain 59..70
FT /label= Partial_BH3_domain
FT /note= "BH3 domain in the full-length BAX alpha consists
FT Misc-difference 55
FT of amino acids 59-73"
FT
FT Misc-difference 55
FT /note= "Wild type Ser is substituted by Ala"
FT MISC-difference 60
FT /note= "Wild type Ser is substituted by Ala"
XX
XX WO200023083-A1.
XX
XX 27-APR-2000.
XX
XX 22-OCT-1999; 99WO-US24747.
XX
XX 22-OCT-1999; 98US-0177315.
XX

PA (UNIT1) UNIV WASHINGTON.
XX Johnson EM, Easton R;
XX WPI: 2000-339513/29.
DR N-PSDB: AAD00124.
XX
PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
PT for the treatment of nervous system disorders -
XX
PS Claim 4: Page 34: 43pp; English.
XX
CC The present sequence is a specifically claimed truncated BAX protein,
CC tBAX70 mutant (tBAX70M) which inhibits neuronal apoptosis induced by
CC trophic factor deprivation. The protein consists of the N-terminal
CC region and a portion of BH3 domain from mouse BAX alpha.
CC It lacks the BH1, BH2 and C-terminal transmembrane
CC domains of the full-length BAX alpha. The tBAX protein lacking only the
CC transmembrane domain has been shown to have anti-apoptotic activity.
CC The present sequence is used to treat diseases associated with neuronal
CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
CC spinal cord injury, head trauma and stroke.
XX
SQ Sequence 70 AA:

Query Match 47.4%; Score 9; DB 21; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GGPTSSSEQI 19
| | | | | | | | | |
Db 11 GGPTSSSEQI 19

RESULT 9
AAV70818
ID AAV70818 standard; Protein: 78 AA.

AC AAV70818;
XX

DT 31-JUL-2000 (first entry)
XX

DE Human neuroprotective truncated BAX protein, tBAX78.
XX

KM Human: truncated BAX protein: tBAX78: BAX alpha; BCL-2 family;
KM neuron: anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
KM apoptosis: treatment; neurodegenerative disease; peripheral nerve injury;
KM spinal cord injury; head trauma; stroke.
XX

OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT Region 1..58
FT /note= "N-terminal region of BAX alpha"
FT 59..73
FT Domain /label= BH3_domain
XX

PN WO200023083-A1.
XX

PD 27-APR-2000.
XX

PF 22-OCT-1999; 99WO-US24747.
XX

PR 22-OCT-1998; 98US-0177315.
XX

PA (UNIT1) UNIV WASHINGTON.
XX

PI Johnson EM, Easton R;
XX

DR WPI: 2000-339513/29.
XX

PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
PT for the treatment of nervous system disorders -

XX
PS Claim 4: Page 33: 43pp; English.
XX

CC The present sequence is a specifically claimed truncated BAX protein
CC tBAX78 which inhibits neuronal apoptosis induced by trophic factor
CC deprivation. The protein consists of first 78 amino acids of human
CC BAX alpha, that includes the N-terminal region and BH3
CC domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of
CC the full-length BAX alpha. The tBAX protein lacking only the
CC transmembrane domain has been shown to have anti-apoptotic activity.
CC The present sequence is used to treat diseases associated with neuronal
CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
CC spinal cord injury, head trauma and stroke.
XX

SQ Sequence 78 AA:
Query Match 47.4%; Score 9; DB 21; Length 78;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GGPTSSSEQI 19
| | | | | | | | | |
Db 11 GGPTSSSEQI 19

RESULT 10
AAV70819
ID AAV70819 standard; Protein: 78 AA.

AC AAV70819;
XX

DT 31-JUL-2000 (first entry)
XX

DE Mouse neuroprotective truncated BAX protein, tBAX78.
XX

KM Mouse: truncated BAX protein: tBAX78: BAX alpha; BCL-2 family;
KM neuron: anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
KM apoptosis: treatment; neurodegenerative disease; peripheral nerve injury;
KM spinal cord injury; head trauma; stroke.
XX

OS Mus musculus.
XX

FH Key Location/Qualifiers
FT Region 1..58
FT /note= "N-terminal region of BAX alpha"
FT 59..73
FT Domain /label= BH3_domain
XX

PN WO200023083-A1.
XX

PD 27-APR-2000.
XX

PF 22-OCT-1999; 99WO-US24747.
XX

PR 22-OCT-1998; 98US-0177315.
XX

PA (UNIT1) UNIV WASHINGTON.
XX

PI Johnson EM, Easton R;
XX

DR WPI: 2000-339513/29.
XX

DR N-PSDB: AAD00123.
XX

PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
PT for the treatment of nervous system disorders -
XX
PS Claim 4: Page 33: 43pp; English.
XX

CC The present sequence is a specifically claimed truncated BAX protein
CC tBAX78 which inhibits neuronal apoptosis induced by trophic factor
CC deprivation. The protein consists of first 78 amino acids of mouse
CC BAX alpha, that includes the N-terminal region and BH3
CC domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of

CC the full-length BAX alpha. The tBAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The present sequence is used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.
 XX
 SQ Sequence 78 AA;

Query Match 47.4%; Score 9; DB 21; Length 78;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GGPTSSSEQI 19
 |||||
 Db 11 GGPTSSSEQI 19

RESULT 11
 AAY70822

ID AAY70822 standard; Protein: 78 AA.

XX AAY70822;

DT 31-JUL-2000 (first entry)

XX Human neuroprotective truncated BAX protein tBAX78 mutant.

KW Human: truncated BAX protein; tBAX78M; BAX alpha; BCL-2 family; mutant;
 KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
 KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 KW spinal cord injury; head trauma; stroke.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 55 /note= "Wild type Ser is substituted by Ala"

FT Misc-difference 60 /note= "Wild type Ser is substituted by Ala"

FT Region 71..78 /note= "sequence not found in BAX alpha"

XX WO200023083-A1.

XX 27-APR-2000.

PF 22-OCT-1999; 99WO-US24747.

PR 22-OCT-1998; 98US-0177315.

XX (UNIW) UNIV WASHINGTON.

PA Johnson EM, Easton R;

XX WPI; 2000-339513/29.

DR N-PSDB; AAD00125.

XX Truncated BAX polypeptides useful for preventing apoptosis of neurons
 PT for the treatment of nervous system disorders -
 XX
 PS Claim 4; Page 34; 43pp; English.

CC The present sequence is a specifically claimed truncated BAX protein,
 CC tBAX78 mutant (tBAX78M) which inhibits neuronal apoptosis induced by
 CC trophic factor deprivation. The protein consists of the N-terminal
 CC region and a portion of BH3 domain of human BAX alpha, and a novel
 CC C-terminal sequence of 8 amino acids not present in BAX alpha.
 CC It lacks the BH1, BH2 and C-terminal transmembrane
 CC domains of the full-length BAX alpha. The tBAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The present sequence is used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,

CC spinal cord injury, head trauma and stroke.
 XX
 SQ Sequence 78 AA;

Query Match 47.4%; Score 9; DB 21; Length 78;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GGPTSSSEQI 19
 |||||
 Db 11 GGPTSSSEQI 19

RESULT 12
 AAY70823

ID AAY70823 standard; Protein: 78 AA.

XX AAY70823;

DT 31-JUL-2000 (first entry)

XX Mouse neuroprotective truncated BAX protein tBAX78 mutant.

KW Mouse; truncated BAX protein; tBAX78M; BAX alpha; BCL-2 family; mutant;
 KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
 KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 KW spinal cord injury; head trauma; stroke.
 XX
 OS Mus musculus.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 55 /note= "Wild type Ser is substituted by Ala"

FT Misc-difference 60 /note= "Wild type Ser is substituted by Ala"

FT Region 71..78 /note= "sequence not found in BAX alpha"

XX WO200023083-A1.

XX 27-APR-2000.

PF 22-OCT-1999; 99WO-US24747.

PR 22-OCT-1998; 98US-0177315.

XX (UNIW) UNIV WASHINGTON.

PA Johnson EM, Easton R;

XX WPI; 2000-339513/29.

DR N-PSDB; AAD00126.

XX Truncated BAX polypeptides useful for preventing apoptosis of neurons
 PT for the treatment of nervous system disorders -
 XX
 PS Claim 4; Page 34-35; 43pp; English.

CC The present sequence is a specifically claimed truncated BAX protein,
 CC tBAX78 mutant (tBAX78M) which inhibits neuronal apoptosis induced by
 CC trophic factor deprivation. The protein consists of the N-terminal
 CC region and a portion of BH3 domain of mouse BAX alpha, and a novel
 CC C-terminal sequence of 8 amino acids not present in BAX alpha.
 CC It lacks the BH1, BH2 and C-terminal transmembrane
 CC domains of the full-length BAX alpha. The tBAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The present sequence is used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.
 XX

SQ Sequence 78 AA;

Query Match 47.4%; Score 9; DB 21; Length 78;
 Best Local Similarity 100.0%; Pred. No. 0.089;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GGPTSSSEQI 19
 |||||
 DB 11 GGPTSSSEQI 19

RESULT 13
 AAY34149
 ID AAY34149 standard; Protein; 131 AA.
 XX AAY34149;
 AC AAY34149;
 XX 30-NOV-1999 (first entry)
 DT 30-NOV-1999 (first entry)
 XX Human truncated Bax protein.
 DE Human truncated Bax protein.
 XX Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy.
 KW Homo sapiens.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Domain 59..101
 FT /note="Portion of BH3 domain essential for dimerisation"
 FT /note="Portion of BH3 domain essential for dimerisation"
 XX MO9946371-A2.
 PN 16-SEP-1999.
 PD 16-SEP-1999.
 XX 11-MAR-1999; 99WO-US05359.
 PF 11-MAR-1999; 99WO-US05359.
 XX 11-MAR-1998; 98US-0077541.
 PR 11-MAR-1998; 98US-0077541.
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX McDonnell TJ, Swisher SG, Fang B, Bruckheimer EM, Sarkiss MG;
 PI Ji L, Roth JA;
 DR WPT: 1999-551404/46.
 DR N-PSDB: AA219763.
 XX New adenovirus vectors, used for killing or inhibiting the growth of
 PT cells and for treating cancers -
 PS Claim 26: Page 148-149; 151pp: English.

This sequence represents a human truncated Bax protein. The cDNA contains a single base deletion relative to the wild-type (AA219764), causing a frameshift which leads to translation of a premature stop codon, resulting in a truncated protein. However, the domain responsible for its function is still present in the truncated protein. Bax (Bcl-2 associated X protein) is a proapoptotic member of the Bcl-2 gene family. Bax functions as a primary response gene in the p53-regulated apoptotic pathway. The Bax gene promoter has 4 p53 binding sites and the expression of Bax is upregulated at the transcriptional level by p53, and Bax mRNA and protein expression have been shown to increase following induction of p53. Bax protein can function as a homodimer, or it can heterodimerise with other Bcl-2 gene family members such as the antiapoptotic protein Bcl-2. Heterodimerisation of Bcl-2 family members provides a means of controlling cell death via the "rheostat" model. This model suggests that the relative amounts of Bcl-2 and Bax determine the susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess, Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is in excess, however, Bax homodimers predominate and the cell becomes susceptible to apoptosis following exposure to an apoptotic stimulus. Additionally, Bax can function in its monomeric form to accelerate cell death. Use of novel adenoviral vectors containing this Bax gene may augment and complement wild-type p53 gene therapy, which induces a G1 cell cycle arrest and/or apoptosis in malignant cells carrying p53 mutations. In addition, Bax overexpression could provide the apoptotic effect of p53 without the need for p53 itself.

XX SQ Sequence 131 AA;
 Query Match 47.4%; Score 9; DB 20; Length 131;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GGPTSSSEQI 19
 |||||
 DB 11 GGPTSSSEQI 19

RESULT 14
 AAR71406
 ID AAR71406 standard; Protein; 192 AA.
 XX AAR71406;
 AC AAR71406;
 XX 15-NOV-1995 (first entry)
 DT 15-NOV-1995 (first entry)
 XX Human Bax protein.
 DE Human Bax protein.
 XX Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line;
 KW apoptosis; membrane-associated cytoplasmic protein; B cell; T cell;
 KW proliferation; cell cycle progression; Bax; apoptotic cell death;
 KW apoptosis; cytokine; death repressor; BH1; BH2; cancer therapy;
 KW hyperplasia; immunodeficiency disease; AIDS; neurodegeneration;
 KW ischaemic cell death.
 XX Homo sapiens.
 OS Homo sapiens.
 XX MO9505750-A.
 PN 02-MAR-1995.
 PD 02-MAR-1995.
 XX 24-AUG-1994; 94WO-US09701.
 PF 24-AUG-1994; 94WO-US09701.
 XX 26-AUG-1993; 93US-0112208.
 PR 25-MAY-1994; 94US-0248819.
 XX (UNIW) UNIV WASHINGTON.
 PA (UNIW) UNIV WASHINGTON.
 XX Korsmeyer SJ;
 PI Korsmeyer SJ;
 DR WPT: 1995-106605/14.
 DR N-PSDB: AAQ97606.
 XX Methods for producing and identifying mutant bcl-2 proteins -
 PT that lack death repressor activity and/or lacks binding to Bax.
 PS Disclosure; Fig 3; 133pp: English.

This sequence represents human Bax protein. Bax is a protein which is associated with the human bcl-2 alpha and beta proteins, the sequences of which are given in AAR71404-05 respectively. bcl-2 is encoded by a proto-oncogene and is capable of inhibiting apoptosis in many hematopoietic cell systems. bcl-2 is a 26 kD membrane-associated cytoplasmic protein and is thought to function by enhancing the survival of hematopoietic cells of B and T origins rather than directly promoting proliferation of these cell types. bcl-2 has not been shown to directly promote cell cycle progression nor does it necessarily alter the dose response to limiting concentrations of IL-3. bcl-2 has been shown to form heterodimers with this 21 kD protein, Bax. Overexpressed Bax accelerates apoptotic cell death induced by cytokine deprivation in an IL-3 dependent cell line, and it also acts to counter the death repressor activity of bcl-2. Therefore, the ratio between bcl-2 and Bax determines cell survival or death following an apoptotic stimulus. The invention gives a mutant form of bcl-2 in which there is at least one amino acid substitution or deletion in the BH1 or BH2 domains. This makes the mutant protein substantially incapable of binding Bax and/or incapable of death repressor activity. Down regulation of bcl-2 is useful in cancer therapy, controlling hyperplasias and eliminating self-reactive clones in autoimmunity by favouring death effector molecules. Up

CC regulating bcl-2 is beneficial in treatment and diagnosis of immuno-
 CC deficiency diseases, including AIDS and neurodegenerative and ischaemic
 CC cell death.

SO Sequence 192 AA;

Query Match 47.4%; Score 9; DB 16; Length 192;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GGPTSSSEOI 19
 |||||
 Db 11 GGPTSSSEOI 19

RESULT 15

AAK71407
 ID AAK71407 standard; Protein; 192 AA.

AC AAK71407;

DT 15-NOV-1995 (first entry)

DE Murine Bax protein.

XX Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line;
 KW apoptosis; membrane-associated cytoplasmic protein; B cell; T cell;
 KW proliferation; cell cycle progression; Bax; apoptotic cell death;
 KW apoptosis; cytokine; death repressor; BH1; BH2; cancer therapy;
 KW hyperplasia; immunodeficiency disease; AIDS; neurodegeneration;
 KW ischaemic cell death.

XX Mus musculus.

OS WO9505750-A.

PN 02-MAR-1995.

PD 24-AUG-1994; 94WO-US09701.

PF 26-AUG-1993; 93US-0112208.

PR 25-MAY-1994; 94US-0248819.

XX (UNIW) UNIV WASHINGTON.

PA Korsmeyer SJ;

PI WPI; 1995-106605/14.

XX Methods for producing and identifying mutant bcl-2 proteins -

PT that lack death repressor activity and/or lacks binding to Bax.

XX Disclosure; Fig 3; 133pp; English.

XX This sequence represents murine Bax protein. Bax is a protein which is
 CC associated with the bcl-2 alpha and beta proteins. bcl-2 is encoded by a
 CC proto-oncogene and is capable of inhibiting apoptosis in many
 CC hematopoietic cell systems. bcl-2 is a 26 kD membrane-associated
 CC cytoplasmic protein and is thought to function by enhancing the survival
 CC of hematopoietic cells of B and T origins rather than directly promoting
 CC proliferation of these cell types. bcl-2 has not been shown to directly
 CC promote cell cycle progression nor does it necessarily alter the dose
 CC response to limiting concentrations of IL-3. bcl-2 has been shown to form
 CC heterodimers with this 21 kD protein, Bax. Overexpressed Bax accelerates
 CC apoptotic cell death induced by cytokine deprivation in an IL-3 dependent
 CC cell line, and it also acts to counter the death repressor activity of
 CC bcl-2. Therefore, the ratio between bcl-2 and Bax determines cell
 CC survival or death following an apoptotic stimulus. The invention gives
 CC a mutant form of bcl-2 in which there is at least one amino acid
 CC substitution or deletion in the BH1 or BH2 domains. This makes the
 CC mutant protein substantially incapable of binding Bax and/or incapable
 CC of death repressor activity. Down regulation of bcl-2 is useful in
 CC cancer therapy, controlling hyperplasias and eliminating self-reactive

CC clones in autoimmunity by favouring death effector molecules. Up
 CC regulating bcl-2 is beneficial in treatment and diagnosis of immuno-
 CC deficiency diseases, including AIDS and neurodegenerative and ischaemic
 CC cell death.

SO Sequence 192 AA;

Query Match 47.4%; Score 9; DB 16; Length 192;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GGPTSSSEOI 19
 |||||
 Db 11 GGPTSSSEOI 19

Search completed: January 7, 2003, 12:38:30
 Job time : 31.2051 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:36:33 : Search time 25.641 Seconds
(without alignments)
160.717 Million cell updates/sec

Title: US-09-876-204-3

Perfect score: 20

Sequence: 1 MDGSGEOPRGCGPTSSSEQIM 20

Scoring table:

Gapop 60.0 , Capext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_21: *
1: sp.archaea: *
2: sp.bacteria: *
3: sp.fungi: *
4: sp.human: *
5: sp.invertebrate: *
6: sp.mammal: *
7: sp.mhc: *
8: sp.organelle: *
9: sp.phage: *
10: sp.plant: *
11: sp rodent: *
12: sp.virus: *
13: sp.vertebrate: *
14: sp.unclassified: *
15: sp.virus: *
16: sp.bacteriap: *
17: sp.archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query length	DB ID	Description
1	20	100.0	24	4 Q8WXU1	Q8WXU1 homo sapien
2	20	100.0	164	4 Q9UQD6	Q9UQD6 homo sapien
3	20	100.0	179	4 Q9NYG7	Q9NYG7 homo sapien
4	12	60.0	192	6 Q8S043	Q8S043 felis silve
5	10	50.0	24	11 Q8VHY7	Q8VHY7 mus musculi
6	9	45.0	743	10 Q9M221	Q9M221 arabidopsis
7	8	40.0	531	4 Q9Y3X0	Q9Y3X0 homo sapien
8	7	35.0	11	11 Q9R0K9	Q9R0K9 mus musculi
9	7	35.0	304	5 Q9N357	Q9N357 caenorhabdi
10	7	35.0	541	10 Q9S7V5	Q9S7V5 arabidopsis
11	7	35.0	589	5 Q18658	Q18658 trypanosoma
12	7	35.0	748	10 Q8W2R7	Q8W2R7 oryza sativ
13	7	35.0	968	3 P87199	P87199 ustillaogo ma
14	7	33.0	1217	4 Q60336	Q60336 homo sapien
15	6	30.0	45	4 Q9H039	Q9H039 homo sapien
16	6	30.0	60	16 Q93JL2	Q93JL2 streptomyces

17	6	30.0	87	8 Q9TKV0	Q9TKV0 nephroselm1
18	6	30.0	91	5 Q9V7F3	Q9V7F3 drosophila
19	6	30.0	94	3 Q12583	Q12583 canidia mal
20	6	30.0	101	10 Q9FSV9	Q9FSV9 equisetum h
21	6	30.0	137	12 Q910X8	Q910X8 human astro
22	6	30.0	137	17 Q9YE12	Q9YE12 aeropyrum p
23	6	30.0	139	10 Q9PPB4	Q9PPB4 oryza sativ
24	6	30.0	169	10 Q81993	Q81993 kalanchoe f
25	6	30.0	193	4 Q9HBR0	Q9HBR0 homo sapien
26	6	30.0	194	4 Q8WVT5	Q8WVT5 homo sapien
27	6	30.0	201	2 Q9RC72	Q9RC72 bacillus ha
28	6	30.0	210	10 Q94113	Q94113 oryza sativ
29	6	30.0	217	4 Q43770	Q43770 homo sapien
30	6	30.0	217	4 Q8WU20	Q8WU20 homo sapien
31	6	30.0	217	11 Q08664	Q08664 mus musculi
32	6	30.0	232	10 Q8VX68	Q8VX68 solenangis
33	6	30.0	237	10 Q8VXN2	Q8VXN2 cupressus s
34	6	30.0	237	10 Q8VX43	Q8VX43 taxus sp. h
35	6	30.0	238	10 Q8W2P2	Q8W2P2 ananas com
36	6	30.0	241	10 Q8VXG5	Q8VXG5 leptotes di
37	6	30.0	243	2 Q9F1Q4	Q9F1Q4 thermus the
38	6	30.0	246	12 Q9JE41	Q9JE41 herpesvirus
39	6	30.0	255	5 Q9V3W7	Q9V3W7 drosophila
40	6	30.0	259	10 Q9M476	Q9M476 dendrobium
41	6	30.0	297	4 Q9BTV5	Q9BTV5 homo sapien
42	6	30.0	297	13 Q08107	Q08107 xenopus lae
43	6	30.0	302	3 Q99034	Q99034 trichoderma
44	6	30.0	305	10 Q96566	Q96566 hydrilla ve
45	6	30.0	310	4 Q9NX73	Q9NX73 homo sapien

ALIGNMENTS

```
RESULT 1
Q8WXU1
ID Q8WXU1 PRELIMINARY: PRT: 24 AA.
AC Q8WXU1;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE BCL2-associated x protein (Fragment).
GN BAX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Thorndorff E.C., Schwartzfarb E.M., Manfredi J.J.;
RT "A conserved intronic response element mediates direct p53-dependent
RT transcriptional activation of both the human and murine bax genes.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF339054; AAL73333.1; -.
FT NON_TER. 24
FT SEQUENCE 24 AA; 2379 MW; 8C3D3E8B7479B798 CRC64;
SQ
Query Match 100.0%; Score 20; DB 4; Length 24;
Best local Similarity 100.0%; Pred. No. 8.2e-15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MDGSGEOPRGCGPTSSSEQIM 20
Db 1 MDGSGEOPRGCGPTSSSEQIM 20
QY 1 MDGSGEOPRGCGPTSSSEQIM 20
Db 1 MDGSGEOPRGCGPTSSSEQIM 20
QY 2
Db 2
QY Q9UQD6 PRELIMINARY: PRT: 164 AA.
AC Q9UQD6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
```

```

DE Bax epsilon.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=BRAIN.
RA MBL:AF007826; PubMed=99120940; PubMed=9920818;
RA Shi B., Triebel D., Kajiji S., Iwata K.R., Bruskin A., Mahajna J.,
RT "Identification and characterization of baxepsilon, a novel bax
RT variant missing the BH2 and the transmembrane domains."
RL Biochem. Biophys. Res. Commun. 254:779-785(1999).
DR EMBL: AF007826; AAD22706.1; -.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PSS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01259; BH3; 1.
SQ SEQUENCE 164 AA; 18129 MW; 12CDB8073EF4C9E CRC64;

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Query Match 100.0%; Score 20; DB 4; Length 164;
Best Local Similarity 100.0%; Pred. No. 4.8e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDGSGEOPRGCGPTSSSEQIM 20
Db 1 MDGSGEOPRGCGPTSSSEQIM 20

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RESULT 3
Q9NYG7 PRELIMINARY; PRT; 179 AA.
AC Q9NYG7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Bax-sigma.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RA MEDLINE=20237095; PubMed=10772918;
RA Schmitt E., Paquet C., Beauchemin M., Dever-Bertrand J., Bertrand R.,
RT "Characterization of bax-sigma, a cell death-inducing isoform of
RT Bax."
RL Biochem. Biophys. Res. Commun. 270:868-879(2000).
DR EMBL: AF247393; AAF71267.1; -.
DR HSSP: 007817; IMA2.
DR InterPro: IPR000712; Bcl2_BH.
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PSS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01259; BH3; 1.
SQ SEQUENCE 179 AA; 19718 MW; 5802B0AC73B2E4CE CRC64;

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Query Match 100.0%; Score 20; DB 4; Length 179;
Best Local Similarity 100.0%; Pred. No. 5.2e-14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDGSGEOPRGCGPTSSSEQIM 20
Db 1 MDGSGEOPRGCGPTSSSEQIM 20

```

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RESULT 4
Q8SO43

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ID Q8SO43 PRELIMINARY; PRT; 192 AA.
AC Q8SO43;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Bax-protein.
GN BAX.
OS Fells silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
OX NCBI_TaxID=9685;
RN [1]
RN SEQUENCE FROM N.A.
RA Yamazaki J., Oguma K., Kano R., Hasegawa A.;
RT "Molecular cloning of feline bcl-2 family."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB080724; BAB85810.1; -.
SQ SEQUENCE 192 AA; 21283 MW; 852D271AE86923FB CRC64;

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Query Match 60.0%; Score 12; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDGSGEOPRGCG 12
Db 1 MDGSGEOPRGCG 12

```

```

RESULT 5
Q8VHY7 PRELIMINARY; PRT; 24 AA.
AC Q8VHY7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Bcl2-associated X protein (Fragment).
GN BAX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RA STRAIN=BA1B/C;
RA Thornborough E.C., Schwartzfarb E.M., Manfredi J.J.;
RT "A conserved intronic response element mediates direct p53-dependent
RT transcriptional activation of both the human and murine bax genes."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF339055; AAL73334.1; -.
PT NON_TER
SQ SEQUENCE 24 AA; 2326 MW; 998C7E8B7479A6CC CRC64;

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Query Match 50.0%; Score 10; DB 11; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 11 GGPSSSEQIM 20
Db 11 GGPSSSEQIM 20

```

```

RESULT 6
Q9M221 PRELIMINARY; PRT; 743 AA.
AC Q9M221;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 82.6 kDa protein.
GN TB10.40.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

```

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OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,
  Lemcke K., Mayer K.F.X., Queller F., Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL138646; CAB81824.1; -.
DR InterPro: IPR000977; DNA_Ligase.
DR PROSITE: PS00697; DNA_LIGASE_A1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 743 AA; 82639 MW; EB30CA4906AC06E2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 9; DB 10; Length 743;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SGEOPRGCG 12
DB 725 SGEOPRGCG 733

RESULT 7
O9Y3X0 PRELIMINARY; PRT; 531 AA.
AC O9Y3X0;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical 59.7 kDa protein (DKFZP586M1019 protein).
GN DKFZP586M1019.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=UTERUS;
RA Wamplit R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050284; CAB43385.1; -.
DR EMBL; BC002787; AAH02787.1; -.
DR EMBL; BC009743; AAH09743.1; -.
KW Hypothetical protein.
SQ SEQUENCE 531 AA; 59703 MW; DE6C474F3253C30C CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 4; Length 531;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGEOPRGCG 12
DB 117 GGEOPRGCG 124

RESULT 8
O9ROK9 PRELIMINARY; PRT; 11 AA.
AC O9ROK9;

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DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Bcl-2 associated x protein (Fragment).
GN BAX OR BAX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20035745; PubMed=10570968;
RX Igata E., Inoue T., Ohtani-Fujita N., Sowa Y., Tsujimoto Y., Sakai T.;
RT "Molecular cloning and functional analysis of the murine bax gene
  promoter.";
RL Gene 238;407-415(1999).
DR EMBL; AB029557; BAA82406.1; -.
DR MGD; MGI:99702; Bax.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1037 MW; 90AAB34E36DB1865 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 11; Length 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQ 7
DB 1 MDGSGEQ 7

RESULT 9
O9N357 PRELIMINARY; PRT; 304 AA.
ID O9N357;
AC O9N357;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Y55F3AR.2 protein.
GN Y55F3AR.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RT None;
RT "Genome sequence of the nematode C. elegans: a platform for
  investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024827; AAF60805.1; -.
DR HSSP; P80028; ITOF.
DR InterPro: IPR000063; Thioled.
DR Pfam: PF00085; Thioled. 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KW Redox-active center.
SQ SEQUENCE 304 AA; 32189 MW; 1ABDE8A81F854A86 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 5; Length 304;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QPRGCGP 13
DB 261 QPRGCGP 267

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RESULT 10
ID 0987V5 PRELIMINARY; PRT; 541 AA.
AC 0987V5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE T16011.4 protein (AT3G09000/T16011_4).
GN T16011.4 OR M2B10.3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLOMBIA.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Niernan W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC T16011 genomic sequence.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, COLOMBIA.
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Niernan W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III PL M2B10 genomic sequence.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Saitou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamanura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC010871; AF07827.1; -
DR EMBL: AC009326; AAD56316.1; -
DR EMBL: AF428276; AAL16108.1; -
SQ SEQUENCE 541 AA; 56813 MW; 3AFE15AD4EADAGE CRC64;

Query Match 35.0%; Score 7; DB 10; Length 541;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RGGGPTS 15
Db 342 RGGGPTS 348
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RESULT 11
ID 018658 PRELIMINARY; PRT; 589 AA.
AC 018658;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE 01-JAN-1998 (TREMBlrel. 05, Last annotation update)
DE PAR3.
GN PAR3B OR PAR3C OR PAR3A.
OS Trypanosoma cruzi.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5693;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ESMERALDO;
RA -Fouts D.L., Miller M.J., Manning J.E.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF005193; AAC32020.1; -
DR EMBL: AF005193; AAC32018.1; -
DR EMBL: AF005194; AAC32019.1; -
SQ SEQUENCE 589 AA; 68748 MW; 55950C0B59359F19 CRC64;

Query Match 35.0%; Score 7; DB 5; Length 589;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GSGEGPR 9
Db 572 GSGEGPR 578
|||||

RESULT 12
ID 08W2R7 PRELIMINARY; PRT; 748 AA.
AC 08W2R7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative wall-associated protein kinase.
GN OSJBA0028C16.5.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Wing R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
RA Saski C., Henry D., Oates R., Simmons J.;
RT "Rice Genomic Sequence.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC098565; AA169423.1; -
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF-like.
DR InterPro: IPR000719; Euk.pkinase.
DR InterPro: IPR002290; Ser_thr.pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00181; EGF; 2.
DR SMART: SM00001; EGF-like; 2.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TYKc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE: PS01187; EGF_CA; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW kinase.
SQ SEQUENCE 748 AA; 82540 MW; 50BF15F0791A12E CRC64;

Query Match 35.0%; Score 7; DB 10; Length 748;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 QPRGGCP 13
Db 343 QPRGGCP 349
|||||

RESULT 13
ID P87199 PRELIMINARY; PRT; 968 AA.
AC P87199;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Kinesin motor protein.

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GN KIN2.
 OS Ustilago maydis (Smut fungus).
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 OX NCB1_TaxId=5270;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97361828; PubMed-9218789;
 RA Lehmler C., Steinberg G., Sneltselaar K.M., Schliwa M., Kahmann R.,
 Bolker M.;
 RT "Identification of a motor protein required for filamentous growth in
 Ustilago maydis.";
 RL EMBO J. 16:3464-3473(1997).
 DR EMBL: U92845; AAB53337.1; -.
 DR HSSP: P33176; 1BG2.
 DR InterPro: IPR001752; kinesin_motor.
 DR Pfam: PF00225; kinesin; 1.
 DR PRINTS: PR00380; KINESINHEAVY.
 DR SMART: SM00129; KISC; 1.
 DR PROSITE: PS50067; KINESIN_MOTOR_DOMAIN2; 1.
 KM ATP-binding: Coiled coil; Microtubules; Motor protein.
 SO SEQUENCE 968 AA; 107472 MW; 3A3B282020D298ED CRC64;

Query Match 35.0%; Score 7; DB 3; Length 968;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 RGGGPTS 15
 DB 921 RGGGPTS 927

RESULT 14
 ID 060336 PRELIMINARY; PRT; 1217 AA.
 AC 060336;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE KIAA0596 protein (Fragment).
 GN KIAA0596.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCB1_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE-98290545; PubMed-9628581;
 RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
 Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:31-39(1998).
 CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 DR EMBL: AB011168; BAA25522.1; -.
 DR InterPro: IPR002114; HPr_SerP_site.
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 8.
 DR PRINTS: PR00320; GPROTEINBRPT.
 DR SMART: SM00320; WD40; 7.
 DR PROSITE: PS00589; PTS_HPR_SER; UNKNOWN_1.
 DR PROSITE: PS50082; WD_REPEATS_2; 1.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 FT NON_TER 1
 SQ SEQUENCE 1217 AA; 131098 MW; 0BC4F4C66722BEF5 CRC64;

Query Match 35.0%; Score 7; DB 4; Length 1217;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SGEOPRG 10
 DB 838 SGEOPRG 844

RESULT 15
 ID 09H039 PRELIMINARY; PRT; 45 AA.
 AC 09H039;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE Hypothetical 5.1 kDa protein (Fragment).
 GN DKFZP547M14.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCB1_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RA Bioecker H., Boecker M., Brandt P., Mewes H.W., Weil B., Wiemann S.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL512746; CAC21671.1; -.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 45 AA; 5069 MW; 64557BA7DB929B37 CRC64;

Query Match 30.0%; Score 6; DB 4; Length 45;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 TSSEOI 19
 DB 1 TSSEOI 6

Search completed: January 7, 2003, 12:39:50
 Job time : 26.641 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:31:53 : Search time 7.17949 Seconds
(without alignments)
115.541 Million cell updates/sec

Title: US-09-876-204-3

Perfect score: 20

Sequence: 1 MDGSGEQPRGCGPTSSSEQIM 20

Scoring table: OLIGO

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	143	1	BAXD_HUMAN
2	20	100.0	192	1	BAXA_BOVIN
3	20	100.0	192	1	BAXA_HUMAN
4	20	100.0	218	1	BAXB_HUMAN
5	11	55.0	41	1	BAXC_HUMAN
6	11	55.0	192	1	BAXA_RAT
7	10	50.0	192	1	BAXA_MOUSE
8	6	30.0	105	1	YGRM_MICRO
9	6	30.0	120	1	NU3C_NEPO
10	6	30.0	126	1	SMDL_CAEL
11	6	30.0	218	1	RRAS_HUMAN
12	6	30.0	218	1	RRAS_MOUSE
13	6	30.0	265	1	ASPX_HUMAN
14	6	30.0	298	1	V33K_HUMAN
15	6	30.0	337	1	FSA_SHEEP
16	6	30.0	344	1	FSA_BOVIN
17	6	30.0	344	1	FSA_HORSE
18	6	30.0	344	1	FSA_PIG
19	6	30.0	416	1	PKC_MYCLE
20	6	30.0	507	1	CP5G_CANTR
21	6	30.0	519	1	CP5L_CANTR
22	6	30.0	519	1	CP5M_DEBHA
23	6	30.0	521	1	CP5L_CANMA
24	6	30.0	524	1	CP5F_CANTR
25	6	30.0	639	1	HS74_PARLI
26	6	30.0	640	1	SYM_PODAN
27	6	30.0	680	1	YPKL_YEAST
28	6	30.0	790	1	DNLI_ARATH
29	6	30.0	960	1	CAP1_SORBI
30	6	30.0	960	1	CAP2_MESCR
31	6	30.0	960	1	CAP2_SORBI
32	6	30.0	960	1	CAP3_SORBI
33	6	30.0	963	1	CAP_PICAB

ALIGNMENTS

34	6	30.0	964	1	CAP2_AMARP
35	6	30.0	964	1	CAP2_TOBAC
36	6	30.0	966	1	CAP1_MESCR
37	6	30.0	966	1	CAP1_SACHY
38	6	30.0	966	1	CAP2_FLATR
39	6	30.0	966	1	CAP2_FLAU
40	6	30.0	966	1	CAP2_MEDSA
41	6	30.0	967	1	CAP1_FLAPR
42	6	30.0	967	1	CAP1_FLATR
43	6	30.0	967	1	CAP1_SOYBN
44	6	30.0	967	1	CAP2_MAIZE
45	6	30.0	967	1	CAP2_SOYBN

RESULT 1

BAXD_HUMAN	STANDARD:	PRT:	143 AA.
AC	P55269;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DE	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	BAX protein, cytoplasmic isoform delta.		
GN	BAX.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
NC	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=9531797; PubMed=7607685;		
RA	Apte S.S., Mattei M.-G., Olsen B.R.;		
RT	"Mapping of the human BAX gene to chromosome 19q13.3-q13.4 and		
RT	isolation of a novel alternatively spliced transcript, BAX delta.";		
RL	Genomics 26:592-594(1995).		
CC	- SUBCELLULAR LOCATION: Cytoplasmic (Potential).		
CC	- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE		
CC	CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY		
CC	ALTERNATIVE SPLICING.		
CC	- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.		
CC	- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.		
CC	- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
DR	EMBL: U19599; AAC50142.1; -		
DR	Genew: HGNC:959; BAX.		
DR	MTM: 600040;		
DR	InterPro: IPR002475; BCL2_family.		
DR	InterPro: IPR000712; BCL2_BH.		
DR	Pfam: PF00452; Bcl-2; 1.		
DR	SMART: SM00337; BCL; 1.		
DR	PROSITE: PS01080; BH1; 1.		
DR	PROSITE: PS01258; BH2; 1.		
DR	PROSITE: PS50062; BCL2_FAMILY; 1.		
KW	Apopotosis; Alternative splicing.		
FT	DOMAIN 49..69		
FT	DOMAIN 101..116		
FT	DOMAIN 15772..MM; BADE4D71D06A75AB CRC64;		
SQ	SEQUENCE 143 AA: 15772 MM; BADE4D71D06A75AB CRC64;		
Query Match	100.0%; Score 20; DB 1; Length 143;		
Best Local Similarity	100.0%; Pred. No. 9.1e-14;		
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 MDGSGEQPRGCGPTSSSEQIM 20		

Db 1 MDGSGEQPRGGGPTSSQIM 20

RESULT 2
BAXA_BOVIN STANDARD; PRT; 192 AA.

AC 002703;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Holstein; TISSUE-Thymus;
RX MEDLINE=98162580; PubMed=9501056;
RA Reyes R.A., Cockrell G.L.;
RT "Increased ratio of bcl-2/bax expression is associated with bovine
leukemia virus-induced leukemogenesis in cattle.";
RL Virology 242:184-192(1998).

CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY
LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE
CESSATION OF SPERM PRODUCTION (BY SIMILARITY).
CC SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Membrane-bound (By similarity).
CC -1- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO
CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
SPLICING.

CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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CC EMBL: U92569; AAC48806.1; -.
DR HSSP: Q07817; IMAZ.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR Apoptosis; Transmembrane; Alternative splicing.
KW DOMAIN 59 73 BH3.
FT DOMAIN 98 118 BH1.
FT DOMAIN 150 165 BH2.
FT TRANSMEM 172 192 POTENTIAL.
SQ SEQUENCE 192 AA; 21259 MW; 6B4D5BAF1D5F87E CRC64;

Query Match 100.0%; Score 20; DB 1; Length 192;

Best Local Similarity 100.0%; Pred. No. 1,2e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEQPRGGGPTSSQIM 20
Db 1 MDGSGEQPRGGGPTSSQIM 20

RESULT 3
BAXA_HUMAN STANDARD; PRT; 192 AA.

AC 007812;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE-B-cell;
RX MEDLINE=93364978; PubMed=8358790;
RA Oliva Z.N., Millman C.L., Korsmeyer S.J.;
RT "bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
accelerates programmed cell death.";
RL Cell 74:609-619(1993).
RN [2]

CC MUTAGENESIS, AND FUNCTION OF BH3 DOMAIN.
RX MEDLINE=96091131; PubMed=8521816;
RA Chittenden T., Fleming G., Houghton A.B., Edb R.G., Gallo G.J.,
RA Elangovan B., Chinnadurai G., Lutz R.J.;
RT "A conserved domain in Bax, distinct from BH1 and BH2, mediates cell
death and protein binding functions.";
RL EMBO J. 14:5589-5596(1995).
RN [3]

RP VARIANT PLASMACYTOMA GLU-11, VARIANT T-CELL ACUTE LYMPHOBLASTIC
LEUKEMIA ARG-67, AND VARIANT BURKITT LYMPHOMA VAL-108.
RX MEDLINE=98200607; PubMed=9531611;
RA Meljertink J.P.P., Mensink E.J.B.M., Wang K., Sedlak T.W.,
RA Sloetjes A.W., de Witte T., Waksman G., Korsmeyer S.J.;
RT "Hematopoietic malignancies demonstrate loss-of-function mutations of
BAX.";
RL Blood 91:2991-2997(1998).

CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.
CC SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC -1- SUBCELLULAR LOCATION: Membrane-bound
CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- DISEASE: Defects in BAX are found in some cell lines from
hematopoietic malignancies as T-cell acute lymphoblastic leukemia,
Burkitt lymphoma, and plasmacytoma.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L22473; AAA03619.1; -.
DR PIR: A47538; A47538.
DR HSSP: Q07817; 1MAZ.
DR Genew: HGNC:959; BAX.
DR MIM: 600040; -.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR Apoptosis: Anti-oncogene; Transmembrane; Alternative splicing;
KW Disease mutation.
FT DOMAIN 59 73 BH3.
FT DOMAIN 98 118 BH1.
FT DOMAIN 150 165 BH2.
FT TRANSMEM 172 192 POTENTIAL.
FT VARIANT 11 11 G -> E (IN PLASMACYTOMA).
FT VARIANT 67 67 /FTID-VAR_013575.
FT VARIANT 67 67 G -> R (IN T-CELL ACUTE LYMPHOBLASTIC
FT LEUKEMIA; LOSS OF HETERODIMERIZATION WITH
FT BCL-2 OR BCL-X(L)).
FT VARIANT 108 108 /FTID-VAR_007809.
FT VARIANT 108 108 G -> V (IN BURKITT LYMPHOMA; LOSS OF
FT HOMODIMERIZATION).
FT /FTID-VAR_013576.
SQ SEQUENCE 192 AA; 21184 MW; 6C0CDB0A7DBE4994 CRC64;

Query Match 100.0%; Score 20; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDSSGEOPRGCGPTSSEQIM 20
Db | 1 MDSSGEOPRGCGPTSSEQIM 20

RESULT 4
BAXB_HUMAN STANDARD: PRT; 218 AA.
AC 007814;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator BAX, cytoplasmic isoform beta.
GN BAX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=93364978; PubMed=8358790;
RA Oliva Z.N., Millman C.L., Korsmeyer S.J.;
RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
RT accelerates programmed cell death.";
RL Cell 74:609-619(1993).
CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
CC HOMOLOG ELB 19K PROTEIN.
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
CC ELB 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
CC ALTERNATIVE SPLICING.
```

```
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC -1- DOMAIN: INTRACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL: L22474; AAA03620.1; -.
DR PIR: B47538; B47538.
DR HSSP: Q07817; 1MAZ.
DR Genew: HGNC:959; BAX.
DR MIM: 600040; -.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR Apoptosis: Alternative splicing.
KW Apoptosis; Alternative splicing.
FT DOMAIN 59 73 BH3.
FT DOMAIN 98 118 BH1.
FT DOMAIN 150 165 BH2.
SQ SEQUENCE 218 AA; 24220 MW; F69DCD070F960192F CRC64;

Query Match 100.0%; Score 20; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDSSGEOPRGCGPTSSEQIM 20
Db | 1 MDSSGEOPRGCGPTSSEQIM 20

RESULT 5
BAXC_HUMAN STANDARD: PRT; 41 AA.
AC 007815;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE BAX protein, cytoplasmic isoform gamma.
GN BAX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=93364978; PubMed=8358790;
RA Oliva Z.N., Millman C.L., Korsmeyer S.J.;
RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
RT accelerates programmed cell death.";
RL Cell 74:609-619(1993).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
CC ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC -----
DR EMBL: L22475; AAA03621.1; -
DR Genbank: HGNC:959; BAX.
DR MIM: 600040; -
DR Apoptosis: Alternative splicing.
SQ SEQUENCE 41 AA; 4678 MW; D94639AAB927859 CRC64;
Query/Match 55.0%; Score 11; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 3 8e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MDGSGEOPRG 11
DB 1 MDGSGEOPRG 11
RESULT 6
BAXA_RAT STANDARD; PRT; 192 AA.
AC 063690; Q62995; Q64383;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9617871; Pubmed=8600029;
RA Han J., Sabbatini P., Perez D., Rao L., Modha D., White E.;
RT "The E1B 19k protein blocks apoptosis by interacting with and
RT inhibiting the p53-inducible and death-promoting Bax protein.";
RL Genes Dev. 10:461-477(1996).
RN [2]
RP SEQUENCE OF 75-192 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97147318; Pubmed=8994223;
RA Madison D.L., Pfeiffer S.E.;
RT "Cloning of the 3' end of rat bax-alpha and corresponding
RT developmental down-regulation in differentiating primary, cultured
RT oligodendrocytes.";
RL Neurosci. Lett. 220:183-186(1996).
RP STRAIN=Sprague-Dawley; TISSUE=Ovary;
RX MEDLINE=95129487; Pubmed=7828536;
RA Tilly J.L., Tilly K.L., Kenton M.L., Johnson A.L.;
RT "Expression of members of the bcl-2 gene family in the immature rat
RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT cell apoptosis is associated with decreased bax and constitutive
RT bcl-2 and bcl-x-long messenger ribonucleic acid levels.";
RL Endocrinology 136:232-241(1995).
CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
CC HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC -1- SUBCELLULAR LOCATION: Membrane-bound.
CC -1- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO
CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH

CC HIGHEST LEVELS IN THE TESTIS AND OVARY.
CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL: U49729; AAC26327.1; -
DR EMBL: U59184; AAC52998.1; -
DR EMBL: U32098; AAA75200.1; -
DR EMBL: S76511; AAC60700.2; -
DR HSP: P53563; IAF3.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; Bcl2_BH.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL_1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
KW Apoptosis; Transmembrane; Alternative splicing.
FT DOMAIN 59 73 BH3.
FT DOMAIN 98 118 BH1.
FT DOMAIN 150 165 BH2.
FT TRANSMEM 172 192 POTENTIAL.
FT CONFLICT 72 72 S->N (IN REF. 3).
FT CONFLICT 76 76 L->M (IN REF. 2).
FT CONFLICT 126 126 C->Y (IN REF. 2).
FT CONFLICT 149 149 L->F (IN REF. 3).
FT CONFLICT 159 159 D->E (IN REF. 1).
SQ SEQUENCE 192 AA; 21350 MW; 7B3CD198D56F589 CRC64;
Query/Match 55.0%; Score 11; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 10 GGGPTSSFOIM 20
DB 10 GGGPTSSFOIM 20
RESULT 7
BAXA_MOUSE STANDARD; PRT; 192 AA.
AC 007813;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6 X DBA/2;
RX MEDLINE=93364978; Pubmed=8358790;
RA Oliva Z.N., Millman C.L., Korsmeyer S.J.;
RT "bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
RT accelerates programmed cell death.";
RL Cell 74:609-619(1993).

```

CC -! FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
CC HOMOLOG ELB 19K PROTEIN, INDUCES THE RELEASE OF CYTOCHROME C,
CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY
CC LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE
CC CESSATION OF Sperm PRODUCTION.
CC -! SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
CC ELB 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC -! SUBCELLULAR LOCATION: Membrane-bound.
CC -! ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO
CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
CC SPLICING.
CC -! TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC -! DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -! SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -! SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -! SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -! SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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CC -----
DR EMBL: L22472; AAA03622.1; -.
DR HSSP: P53563; IAR3.
DR MGD: MGI:99702; Bax.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL2_BH.
DR Pfam: PF00452; BCL-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS50062; BCL2_FAMILY; 1.
DR Apoptosis; Transmembrane; Alternative splicing.
FT DOMAIN 59 73 BH3.
FT DOMAIN 98 118 BH1.
FT DOMAIN 150 165 BH2.
FT TRASMEN 172 192 POTENTIAL.
SQ SEQUENCE 192 AA; 21394 MW; D2E0B3566579FAFF CRC64;

Query Match 50.0%; Score 10; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSSEQIM 20
DB 11 GGPTSSSEQIM 20
IIIIIIIIII

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RA Kelenen G.H., Dundliffe E., Financesek I.;
RT "Cloning and characterization of gentamicin-resistance genes from
RT Micromonospora purpurea and Micromonospora rosea.";
RL Gene 98:53-60(1991).
CC -----
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CC -----
DR EMBL: M55521; AAA25339.1; -.
DR PIR: PM0018; PM0018.
KW Antibiotic resistance; Hypothetical protein.
FT NON_TER 105 105
SQ SEQUENCE 105 AA; 11112 MW; 56125793440BA48C CRC64;

Query Match 30.0%; Score 6; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSS 16
DB 81 GGPTSS 86
IIIIII

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RESULT 8
YGRM_MICRO
ID YGRM_MICRO STANDARD; PRT; 105 AA.
AC P24621;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in GRM 3' region (Fragment).
OS Micromonospora rosea.
OC Bacteria; Actinobacteria; Actinobacteriales (class); Actinobacteridae;
OC Actinomycetales; Micromonosporinae; Micromonosporaceae;
OC Micromonospora.
OX NCBI_TaxID=1878;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91192615; PubMed=2013410;

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RESULT 9
NU3C_NEPOL
ID NU3C_NEPOL STANDARD; PRT; 120 AA.
AC O9TKX9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE NADH-plastoquinone oxidoreductase chain 3, chloroplast (EC 1.6.5.3).
GN NDHC.
OS Nephroselmis olivacea.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
OC Chlorodendraceae; Chlorodendraceae; Nephroselmis.
OX NCBI_TaxID=31312;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIES-484;
RX MEDLINE=99398694; PubMed=10468594;
RA Turnell M., Otis C., Lemieux C.;
RT "The complete chloroplast DNA sequence of the green alga Nephroselmis
RT olivacea: insights into the architecture of ancestral chloroplast
RT genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10248-10253(1999).
CC -! CATALYTIC ACTIVITY: NADH + plastoquinone = NAD(+) + plastoquinol.
CC -! SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 3 FAMILY.
CC -----
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CC -----
DR EMBL: AF137379; AAD54837.1; -.
DR InterPro: IPR000440; Oxidored_q4.
DR Pfam: PF00507; oxidored_q4; 1.
KW Oxidoreductase; NAD; Plastoquinone; Chloroplast.
SQ SEQUENCE 120 AA; 13680 MW; DF6700BBE9565C7F5 CRC64;

```

```

Query Match 30.0%; Score 6; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PROGCP 13

```

```

Db      33 PRGCGP 38

RESULT 10
SMDL_CAEEL STANDARD; PRT; 126 AA.
AC Q10013;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable small nuclear ribonucleoprotein Sm D1 (snRNP core protein D1)
DE (Sm-D1)
GN T28D9.10.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RL Fillion L.;
RL Submitted (JUN-1995) to the EMBL/Genbank/DDIJ databases.
CC -1- FUNCTION: ESSENTIAL FOR PRE-MRNA SPLICING. IMPLICATED IN THE
CC FORMATION OF STABLE, BIOLOGICALLY ACTIVE SNRNP STRUCTURES
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SNRNP CORE PROTEIN FAMILY.
CC -----
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CC -----
DR EMBL: U28738; AAA68313.1; -
DR WormPep: T28D9.10; CE02065.
DR InterPro: IPR001163; snRNP_Sm.
DR Pfam: PF01423; Sm; 1.
KW Nuclear protein; Ribonucleoprotein; mRNA splicing; mRNA processing.
SO SEQUENCE 126 AA; 15625 MW; 24D26C7FA9DBD65 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PRGCGP 13
Db 119 PRGCGP 124

RESULT 11
RRAS_HUMAN STANDARD; PRT; 218 AA.
ID RRAS_HUMAN
AC P10301;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ras-related protein R-Ras (p23).
DE RAS.
GN RAS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=87078390; PubMed=3098437;
RX Lowe D.G., Capon D.J., Delwart E., Sakaguchi A.Y., Naylor S.L.,
RA Goeddel D.V.;
RT "Structure of the human and murine R-Ras genes, novel genes closely
RT related to ras proto-oncogenes.";
```

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RL Cc11 48:137-146(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC Tissue=Brain, and Uterus;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/Genbank/DDIJ databases.
CC -1- SUBCELLULAR LOCATION: INNER SURFACE OF PLASMA MEMBRANE POSSIBLY
CC WITH ATTACHMENT ROUTING ACYLATION OF THE C-TERMINAL CYSTEINE
CC (BY SIMILARITY WITH RAS).
CC -1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE R-RAS SUB-FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M14949; AAA60256.1; -
DR EMBL: M14948; AAA60256.1; JOINED.
DR EMBL: BC016286; AAH16286.1; -
DR EMBL: BC016318; AAH16318.1; -
DR PIR: A26159; TYHURR.
DR HSSP: P01112; 1PUL.
DR SWISS-2DPAGE: P10301; HUMAN.
DR Genew: HGNC:10447; RAS.
DR MIM: 165090; -
DR InterPro: IPR003577; GTPase_Ras.
DR InterPro: IPR001230; Prenyl_site.
DR InterPro: IPR001806; Ras_trnsfrmng.
DR InterPro: IPR005225; Small_GTP.
DR Pfam: PF00071; Ras; 1.
DR PRINTS: PR00449; RASTRNSFRMNG.
DR SMART: SM00173; Ras; 1.
DR TIGRFAMs: TIGR00231; small_GTP; 1.
KW GTP-binding; Prenylation; Lipoprotein.
FT NP_BIND 36 43 GTP (BY SIMILARITY).
FT NP_BIND 83 87 GTP (BY SIMILARITY).
FT NP_BIND 142 145 GTP (BY SIMILARITY).
FT DOMAIN 58 66 EFECTOR_REGION (BY SIMILARITY).
FT LIPID 215 215 GERANYL-GERANYL (BY SIMILARITY).
SO SEQUENCE 218 AA; 23480 MW; 437F73170670EB28 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PRGCGP 13
Db 14 PRGCGP 19

RESULT 12
RRAS_MOUSE STANDARD; PRT; 218 AA.
ID RRAS_MOUSE
AC P10833;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Ras-related protein R-Ras (p23).
DE RAS.
GN RAS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=87078390; PubMed=3098437;
RX Lowe D.G., Capon D.J., Delwart E., Sakaguchi A.Y., Naylor S.L.,
RA Goeddel D.V.;
RT "Structure of the human and murine R-Ras genes, novel genes closely
RT related to ras proto-oncogenes.";
```

RL Cell 48:137-146(1987).
 CC -1- SUBCELLULAR LOCATION: INNER SURFACE OF PLASMA MEMBRANE POSSIBLY
 CC WITH ATTACHMENT REQUIRING ACYLATION OF THE C-TERMINAL CYSTEINE
 CC (BY SIMILARITY WITH RAS).
 CC -1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE R-RAS SUB-FAMILY.
 CC -----
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 CC -----
 DR EMBL: M21019; AAA0038.1; -
 DR HSSP: P01112; 1PLL.
 DR MGD: MGI:96179; RTas.
 DR InterPro: IPR003577; GTPase_Ras.
 DR InterPro: IPR001230; Prenyl_site.
 DR InterPro: IPR001806; Ras_trnsfmg.
 DR InterPro: IPR005225; Small_GTP.
 DR Pfam: PF00071; Ras_1.
 DR PRINTS: PR00449; RASTRNSFRMG.
 DR SMART: SM00173; RAS; 1.
 DR TIGRfam: TIGR00231; small_GTP; 1.
 KW GTP-binding; Prenylation; Lipoprotein.
 FT NP_BIND 36 43 GTP (BY SIMILARITY).
 FT NP_BIND 83 87 GTP (BY SIMILARITY).
 FT NP_BIND 142 145 GTP (BY SIMILARITY).
 FT DOMAIN 58 66 EFFECTOR REGION (BY SIMILARITY).
 FT LIPID 215 215 GERANYL-GERANYL (BY SIMILARITY).
 SQ SEQUENCE 218 AA; 23764 MW; C1D32CE7904322E5 CRC64;
 Query Match 30.0%; Score 6; DB 1; Length 218;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 8 PROGCP 13
 DB 14 PROGCP 19
 RESULT 13
 ID ASPX_HUMAN STANDARD: PRT; 265 AA.
 AC P26A36;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acrosomal protein SP-10 precursor (Acrosomal vesicle protein-1).
 GN ACRV1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=90268085; PubMed=1693291;
 RA Wright R.M., John E., Klotz K., Flickinger C.J., Herr J.C.;
 RT "Cloning and sequencing of cDNAs coding for the human intra-acrosomal
 antigen SP-10.";
 RL Biol. Reprod. 42:693-701(1990).
 RP [2]
 RP REVISIONS.
 RA Wright R.M., John E., Klotz K., Flickinger C.J., Herr J.C.;
 RL Biol. Reprod. 43:903-903(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93385341; PubMed=8373955;
 RA Wright R.M., Surf A.K., Kornreich B., Flickinger C.J., Herr J.C.;
 RT "Cloning and characterization of the gene coding for the human
 acrosomal protein SP-10.";

RL Biol. Reprod. 49:316-325(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Strausberg R.;
 RN Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP ALTERNATIVE SPLICING.
 RC TISSUE=Testis;
 RX MEDLINE=95344748; PubMed=7619499;
 RA Freeman A.J., Flickinger C.J., Herr J.C.;
 RT "Characterization of alternatively spliced human SP-10 mRNAs.";
 RL Mol. Reprod. Dev. 41:100-108(1995).
 RN [6]
 RP SEQUENCE OF 78-100, 106-122 AND 127-151.
 RX MEDLINE=92345498; PubMed=1637938;
 RA Herr J.C., Klotz K., Shannon J., Wright R.M., Flickinger C.J.;
 RT "Purification and microsequencing of the intra-acrosomal protein
 SP-10. Evidence that SP-10 heterogeneity results from endoproteolytic
 processes.";
 RL Biol. Reprod. 47:11-20(1992).
 CC -1- SUBCELLULAR LOCATION: NASCENT ACROSOMAL VESICLE OF GOLGI PHASE
 CC SPERMATIDS.
 CC -1- ALTERNATIVE PRODUCTS: At least 11 isoforms; 1 (shown here), 2, 3,
 CC 4, 5, 6, 7, 8, 9, 10 and 11; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: TESTIS.
 CC -----
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 CC -----
 DR EMBL: M82967; AAA36625.1; -
 DR EMBL: M82968; AAA36626.1; -
 DR EMBL: S65583; AAB28238.2; -
 DR EMBL: S65606; AAB28238.2; JOINED.
 DR EMBL: S65576; AAB28238.2; JOINED.
 DR EMBL: S65578; AAB28238.2; JOINED.
 DR EMBL: BC014588; AAB14588.1; -
 DR PIR: A37225; A37225.
 DR GeneW: HGNC:127; ACRY1.
 DR MIM: 102525; -
 KW Signal; Glycoprotein; Repeat; Sperm; Alternative splicing.
 FT SIGNAL 1 21
 FT CHAIN 22 265
 FT DOMAIN 66 95
 FT REPEAT 66 70
 FT REPEAT 71 75
 FT REPEAT 91 95
 FT DOMAIN 85 168
 FT REPEAT 85 88
 FT REPEAT 120 123
 FT REPEAT 120 123
 FT REPEAT 145 148
 FT REPEAT 165 168
 FT DOMAIN 110 174
 FT REPEAT 110 114
 FT REPEAT 115 119
 FT REPEAT 125 129
 FT REPEAT 135 139
 FT REPEAT 140 144
 FT REPEAT 150 154
 FT REPEAT 155 159
 FT REPEAT 160 164
 FT REPEAT 170 174
 FT CARBOHYD 258 258
 FT VARSPLIC 41 95
 FT VARSPLIC 41 110
 FT VARSPLIC 41 135
 FT VARSPLIC 41 184
 N-LINKED (GLCNAC...) (POTENTIAL).
 MISSING (IN ISOFORM 3 AND ISOFORM 7).
 MISSING (IN ISOFORM 4, ISOFORM 5, ISOFORM
 8 AND ISOFORM 9).
 MISSING (IN ISOFORM 6).
 MISSING (IN ISOFORM 10).

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FT VARSPLIC 41 224 MISSING (IN ISOFORM 11).
FT VARSPLIC 155 155 MISSING (IN ISOFORM 7).
FT VARSPLIC 121 155 MISSING (IN ISOFORM 9).
FT VARSPLIC 166 184 MISSING (IN ISOFORM 2 AND ISOFORM 5).
FT VARSPLIC 185 224 MISSING (IN ISOFORM 8).
FT VARSPLIC 91 91 S -> E (IN REF. 6).
FT CONFLICT 126 126 G -> R (IN REF. 3).
SQ SEQUENCE 265 AA: 28156 MW: 318216453F20D68A CRC64;

Query Match 30.0%; Score 6; DB 1; Length 265;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GSGEOP 8
Db 149 GSGEOP 154

RESULT 14
Y33K_HUMAN STANDARD; PRT; 298 AA.
ID Y33K_HUMAN
AC 004323;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical 33.4 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Pollard K.M.;
RL Submitted (JUN-1991) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 UBA DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 UBX DOMAIN.
CC -----
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CC -----
CC EMBL: M68864; AAA36396.1; -
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR001012; UBX.
DR Pfam: PF00627; UBA; 1.
DR Pfam: PF00789; UBX; 1.
DR SMART: SM00165; UBA; 1.
DR SMART: SM00166; UBX; 1.
KW Hypothetical protein.
SQ SEQUENCE 298 AA: 33396 MW: 6C671CFF4AC15D7 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 PTSSEQ 18
Db 64 PTSSEQ 69

RESULT 15
FSA_SHEEP STANDARD; PRT; 337 AA.
ID FSA_SHEEP
AC P31514;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Follistatin precursor (FS) (Activin-binding protein) (Fragment).
GN FST.

```

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OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92337809; PubMed=1632897;
RA Tisdall D.J., Hill D., Petersen G.B., Fleming J.S.;
RT "Ovine follistatin: characterization of cDNA and expression in sheep
RT ovary during the luteal phase of the oestrous cycle.";
RL J. Mol. Endocrinol. 8:259-264(1992).
CC -1- FUNCTION: BINDS DIRECTLY TO ACTIVIN AND FUNCTIONS AS AN ACTIVIN
CC ANTAGONIST. SPECIFIC INHIBITOR OF THE BIOSYNTHESIS AND SECRETION
CC OF PITUITARY FOLLICLE STIMULATING HORMONE (FSH).
CC -1- SUBUNIT: MONOMER (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: CONTAINS 3 FOLLISTATIN-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 KAZAL-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL: M63123; AAA31522.1; -
DR HSP: P37109; IPCE.
DR InterPro: IPR003645; FOLN.
DR InterPro: IPR002350; kazal.
DR Pfam: PF00050; kazal; 3.
DR SMART: SM00274; FOLN; 3.
DR SMART: SM00280; KAZAL; 3.
DR PROSITE: PS00282; KAZAL; FALSE_NEG.
KW Glycoprotein; Repeat; Signal.
FT NON_TER 1 22
FT SIGNAL 23 337
FT CHAIN 87 110
FT DOMAIN 111 157
FT DOMAIN 160 183
FT DOMAIN 185 232
FT DOMAIN 237 261
FT DOMAIN 263 309
FT DOMAIN 314 326
FT DISULFID 111 143
FT DISULFID 115 136
FT DISULFID 125 157
FT DISULFID 185 218
FT DISULFID 189 211
FT DISULFID 200 232
FT DISULFID 263 295
FT DISULFID 267 288
FT DISULFID 277 309
FT CARBOHYD 117 117
FT CARBOHYD 281 281
SQ SEQUENCE 337 AA: 37082 MW: 1E8BE1BBB6B109C4 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 337;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 PTSSEQ 18
Db 192 PTSSEQ 197

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Search completed: January 7, 2003, 12:38:53
 Job time : 8.17949 secs

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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:37:29 : Search time 11.7949 Seconds
(without alignments)
49.891 Million cell updates/sec

Title: US-09-876-204-3

Perfect score: 20

Sequence: 1 MDGSGEQPRGGPRTSSQIM 20

Scoring table: OLIGO

Gapop 60.0 , Capext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	4	US-09-166-028-3
2	20	100.0	192	1	US-08-112-208C-2
3	20	100.0	192	1	US-08-112-208C-9
4	20	100.0	192	1	US-08-248-819A-2
5	20	100.0	192	1	US-08-248-819A-9
6	20	100.0	192	1	US-08-607-269-25
7	20	100.0	192	1	US-08-471-058-13
8	20	100.0	192	2	US-08-337-646A-2
9	20	100.0	192	2	US-08-337-646A-9
10	20	100.0	192	2	US-08-856-531-2
11	20	100.0	192	2	US-08-856-531-9
12	20	100.0	192	2	US-08-856-034-2
13	20	100.0	192	2	US-08-856-034-9
14	20	100.0	192	3	US-08-471-057-13
15	20	100.0	192	4	US-09-127-048-7
16	20	100.0	192	4	US-08-927-326-2
17	20	100.0	192	4	US-08-927-326-9
18	20	100.0	192	5	PCT-US95-04600-25
19	20	100.0	221	1	US-08-616-732A-9
20	20	100.0	221	4	US-09-037-742B-9
21	15	75.0	25	1	US-08-798-897-21
22	15	75.0	25	2	US-08-978-523-21
23	11	55.0	20	4	US-09-166-028-5
24	11	55.0	41	1	US-08-112-208C-7
25	11	55.0	41	1	US-08-248-819A-7
26	11	55.0	41	2	US-08-337-646A-7
27	11	55.0	41	2	US-08-856-531-7

28	11	55.0	41	2	US-08-856-031-7	Sequence 7, Appl1
29	11	55.0	41	4	US-08-927-326-7	Sequence 7, Appl1
30	10	50.0	20	4	US-09-166-028-4	Sequence 4, Appl1
31	10	50.0	192	1	US-08-112-208C-3	Sequence 3, Appl1
32	10	50.0	192	1	US-08-112-208C-8	Sequence 8, Appl1
33	10	50.0	192	1	US-08-248-819A-3	Sequence 8, Appl1
34	10	50.0	192	1	US-08-248-819A-8	Sequence 8, Appl1
35	10	50.0	192	2	US-08-337-646A-8	Sequence 8, Appl1
36	10	50.0	192	2	US-08-337-646A-3	Sequence 8, Appl1
37	10	50.0	192	2	US-08-856-531-3	Sequence 8, Appl1
38	10	50.0	192	2	US-08-856-531-8	Sequence 8, Appl1
39	10	50.0	192	2	US-08-856-034-3	Sequence 8, Appl1
40	10	50.0	192	2	US-08-856-034-8	Sequence 8, Appl1
41	10	50.0	192	4	US-09-127-048-6	Sequence 6, Appl1
42	10	50.0	192	4	US-08-927-326-3	Sequence 3, Appl1
43	10	50.0	192	4	US-08-927-326-8	Sequence 8, Appl1
44	9	45.0	19	4	US-09-166-028-1	Sequence 1, Appl1
45	6	30.0	120	4	US-09-134-001C-5332	Sequence 5332, Ap

ALIGNMENTS

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RESULT 1
US-09-166-028-3
: Sequence 3, Application US/09166028
: Patent No. 6245885
: GENERAL INFORMATION:
: APPLICANT: Gordon C. Shore et al.
: TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
: FILE REFERENCE: 50013/011001
: CURRENT APPLICATION NUMBER: US/09/166,028
: CURRENT FILING DATE: 1998-10-05
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-166-028-3

Query Match      100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+13;
Matches 20; Conservative 0; Mismatches 0; Indels 0;

QY      1 MDGSGEQPRGGPRTSSQIM 20
Db      1 MDGSGEQPRGGPRTSSQIM 20

RESULT 2
US-08-112-208C-2
: Sequence 2, Application US/08112208C
: Patent No. 5691179
: GENERAL INFORMATION:
: APPLICANT: KORSMEYER, Stanley J.
: TITLE OF INVENTION: CELL DEATH REGULATORS
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourile and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/112,208C
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; FILING DATE: 26-AUG-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-112-208C-2

Query Match          100.0%; Score 20; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSSGEQPRGGGPTSSSEQIM 20
Db 1 MDSSGEQPRGGGPTSSSEQIM 20

RESULT 3
US-08-112-208C-9
; Sequence 9, Application US/08112208C
; Patent No. 5691179
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/112,208C
; FILING DATE: 26-AUG-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-112-208C-9

Query Match          100.0%; Score 20; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSSGEQPRGGGPTSSSEQIM 20
Db 1 MDSSGEQPRGGGPTSSSEQIM 20
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; FILING DATE: 26-AUG-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-248-819A-2

Query Match          100.0%; Score 20; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSSGEQPRGGGPTSSSEQIM 20
Db 1 MDSSGEQPRGGGPTSSSEQIM 20

RESULT 4
US-08-248-819A-2
; Sequence 2, Application US/08248819A
; Patent No. 5700638
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,819A
; FILING DATE: 25-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-248-819A-2

Query Match          100.0%; Score 20; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSSGEQPRGGGPTSSSEQIM 20
Db 1 MDSSGEQPRGGGPTSSSEQIM 20

RESULT 5
US-08-248-819A-9
; Sequence 9, Application US/08248819A
; Patent No. 5700638
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,819A
; FILING DATE: 25-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-248-819A-9

Query Match          100.0%; Score 20; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSSEQIM 20
DB 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 6
US-08-607-269-25
; Sequence 23, Application US/08607269
; Patent No. 5702897
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: Interaction of Proteins Involved in a
; TITLE OF INVENTION: Cell Death Pathway
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/607,269
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/226,876
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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US-08-607-269-25

Query Match          100.0%; Score 20; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSSEQIM 20
DB 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 7
US-08-471-058-13
; Sequence 13, Application US/08471058
; Patent No. 5770443
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Barr, Philip J.
; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
; TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
; TITLE OF INVENTION: THEROF
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,058
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; APPLICATION NUMBER: 08/160,067
; FILING DATE: 30-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lemhardt, Susan K
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-471-058-13

Query Match          100.0%; Score 20; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSSEQIM 20
DB 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 8
US-08-337-646A-2
; Sequence 2, Application US/08337646A
; Patent No. 5856171
; GENERAL INFORMATION:

```

APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,646A
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-337-646A-2

Query Match 100.0%; Score 20; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSSGEOPRGCGPTSSSEQIM 20
DB 1 MDSSGEOPRGCGPTSSSEQIM 20

RESULT 9
US-08-337-646A-9
Sequence 9, Application US/08337646A
Patent No. 5856171
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,646A
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-337-646A-9

Query Match 100.0%; Score 20; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSSGEOPRGCGPTSSSEQIM 20
DB 1 MDSSGEOPRGCGPTSSSEQIM 20

RESULT 10
US-08-856-531-2
Sequence 2, Application US/08856531
Patent No. 594290
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,531
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, Donald R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..192
OTHER INFORMATION: /note= "Human BAX polypeptide"

US-08-856-531-2

Query Match 100.0%; Score 20; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGGPTSSSEQIM 20
Db 1 MDGSGEOPRGGPTSSSEQIM 20

RESULT 11
US-08-856-531-9

; Sequence 9, Application US/08856531
; Patent No. 5942490
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howell & Haferkamp, L.C.
; STREET: 7733 Forsyth Blvd., Suite 1400
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,531
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, Donald R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-6092
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..192
; OTHER INFORMATION: /note= "Human BAX polypeptide"

US-08-856-531-9

Query Match 100.0%; Score 20; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGGPTSSSEQIM 20
Db 1 MDGSGEOPRGGPTSSSEQIM 20

RESULT 12
US-08-856-034-2

; Sequence 2, Application US/08856034
; Patent No. 5955595
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,034
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, Donald R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976175
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

NAME/KEY: Protein
LOCATION: 1..192
OTHER INFORMATION: /note= "Human BAX polypeptide"

US-08-856-034-2

Query Match 100.0%; Score 20; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGGPTSSSEQIM 20
Db 1 MDGSGEOPRGGPTSSSEQIM 20

RESULT 13
US-08-856-034-9

; Sequence 9, Application US/08856034
; Patent No. 5955595
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howell & Haferkamp, L.C.
; STREET: 7733 Forsyth Blvd., Suite 1400
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,034
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, Donald R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976175
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..192
OTHER INFORMATION: /note="Human BAX polypeptide"

Query Match 100.0%; Score 20; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDGSGEQPRGGPTSSSEQIM 20
Db 1 MDGSGEQPRGGPTSSSEQIM 20

RESULT 14

US-08-471-057-13
Sequence 13, Application US/08471057
Patent No. 6015687
GENERAL INFORMATION:
APPLICANT: KIEFER, MICHAEL C.
TITLE OF INVENTION: NOVEL APOPTOSIS-MODULATING PROTEINS, DNA
TITLE OF INVENTION: ENCODING THE PROTEINS AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORRESTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,057
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,157
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: LEHNHARDT, SUSAN K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-057-13

Query Match 100.0%; Score 20; DB 3; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDGSGEQPRGGPTSSSEQIM 20
Db 1 MDGSGEQPRGGPTSSSEQIM 20

RESULT 15

US-09-127-048-7
Sequence 7, Application US/09127048
Patent No. 6165732
GENERAL INFORMATION:
APPLICANT: Schlessinger, Stanley J.
TITLE OF INVENTION: Method for Identifying Apoptosis Modulating Compounds
FILE REFERENCE: 6029-6052
CURRENT APPLICATION NUMBER: US/09/127,048
CURRENT FILING DATE: 1998-07-31
EARLIER APPLICATION NUMBER: 60/061,823
EARLIER FILING DATE: 1997-10-14
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
US-09-127-048-7

Query Match 100.0%; Score 20; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDGSGEQPRGGPTSSSEQIM 20
Db 1 MDGSGEQPRGGPTSSSEQIM 20

Search completed: January 7, 2003, 12:40:52
Job time: 12.7949 secs

XX The present invention describes a pure protein (P1) comprising a BAX
 CC polypeptide lacking an apoptotic regulation of targeting (ART) domain.
 CC P1 has cytostatic activity and can be used in the modulation of
 CC apoptosis. The polypeptides and methods from the present invention are
 CC useful for identifying compounds that modulate apoptosis which can then
 CC be used for treating cancer. The present sequence represents a human
 CC BAX peptide sequence of amino acids 1 to 20, which is used in an
 CC example from the present invention.

SQ Sequence 20 AA:

Query Match 100.0%; Score 20; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSSGEQPRGGGPTSSSQIM 20
 DB 1 MDSSGEQPRGGGPTSSSQIM 20
 ||||||||||||||||||

RESULT 2
 ID AAY70816 standard; Protein: 70 AA.
 XX AAY70816;
 XX 31-JUL-2000 (first entry)

DE Human neuroprotective truncated BAX protein, tBAXX70.
 XX
 XX Human; truncated BAX protein; tBAX70; BAX alpha; BCL-2 family;
 KM neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
 KM apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 KM spinal cord injury; head trauma; stroke.

OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Region 1..58
 FT /note= "N-terminal region of BAX alpha"
 FT 59..70
 FT /label= Partial_BH3_domain
 FT /note= "BH3 domain in the full-length BAX alpha consists
 of amino acids 59-73"

WO200023083-A1.
 XX
 XX PD 27-APR-2000.
 XX
 XX PF 22-OCT-1999; 99WO-US24747.
 XX
 XX PR 22-OCT-1998; 98US-0177315.
 XX
 XX PA (UNITW) UNIV WASHINGTON.
 XX
 XX PI Johnson EM, Easton R;
 XX
 XX DR WPI: 2000-339513/29.
 XX
 XX PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
 PS for the treatment of nervous system disorders -
 XX
 XX Claim 4; Page 32; 43pp; English.
 CC The present sequence is a specifically claimed truncated BAX protein
 CC tBAX70 which inhibits neuronal apoptosis induced by trophic factor
 CC deprivation. The protein consists of first 70 amino acids of human
 CC BAX alpha, that includes the N-terminal region and a portion of the BH3
 CC domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of
 CC the full-length BAX alpha. The tBAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The present sequence is used to treat diseases associated with neuronal

CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.

SQ Sequence 70 AA:

Query Match 100.0%; Score 20; DB 21; Length 70;
 Best Local Similarity 100.0%; Pred. No. 5.3e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSSGEQPRGGGPTSSSQIM 20
 DB 1 MDSSGEQPRGGGPTSSSQIM 20
 ||||||||||||||||||

RESULT 3
 ID AAY70820 standard; Protein: 70 AA.
 XX AAY70820;
 XX 31-JUL-2000 (first entry)

DE Human neuroprotective truncated BAX protein tBAX70 mutant.
 XX
 XX Human; truncated BAX protein; tBAX70M; BAX alpha; BCL-2 family; mutant;
 KM neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
 KM apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 KM spinal cord injury; head trauma; stroke.

OS Homo sapiens.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Region 1..58
 FT /note= "N-terminal region from BAX alpha"
 FT 59..70
 FT /label= Partial_BH3_domain
 FT /note= "BH3 domain in the full-length BAX alpha consists
 of amino acids 59-73"

Misc-difference 55
 FT /note= "Wild type Ser is substituted by Ala"
 FT 60
 FT /note= "Wild type Ser is substituted by Ala"

WO200023083-A1.
 XX
 XX PD 27-APR-2000.
 XX
 XX PF 22-OCT-1999; 99WO-US24747.
 XX
 XX PR 22-OCT-1998; 98US-0177315.
 XX
 XX PA (UNITW) UNIV WASHINGTON.
 XX
 XX PI Johnson EM, Easton R;
 XX
 XX DR WPI: 2000-339513/29.
 XX
 XX PT Truncated BAX polypeptides useful for preventing apoptosis of neurons
 PS for the treatment of nervous system disorders -
 XX
 XX Claim 4; Page 33-34; 43pp; English.
 CC The present sequence is a specifically claimed truncated BAX protein,
 CC tBAX70 mutant (tBAX70M) which inhibits neuronal apoptosis induced by
 CC trophic factor deprivation. The protein consists of the N-terminal
 CC region and a portion of BH3 domain of human BAX alpha.
 CC It lacks the BH1, BH2 and C-terminal transmembrane
 CC domains of the full-length BAX alpha. The tBAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The present sequence is used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.

XX Sequence 70 AA;

Query Match 100.0%; Score 20; DB 21; Length 70;
Best Local Similarity 100.0%; Pred. No. 5.3e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGCGPTSSEQIM 20
|||||
DB 1 MDGSGEOPRGCGPTSSEQIM 20

RESULT 4

AAV70818
ID AAV70818 standard; Protein; 78 AA.

AC AAV70818;

DT 31-JUL-2000 (first entry)

DE Human neuroprotective truncated BAX protein, tBAX78.

KW Human; truncated BAX protein; tBAX78; BAX alpha; BCL-2 family;

KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;

KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;

KW spinal cord injury; head trauma; stroke.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..58 /note= "N-terminal region of BAX alpha"

FT Domain 59..73 /label= BH3_domain

WO200023083-A1.

PD 27-APR-2000.

PF 22-OCT-1999; 99WO-US24747.

PR 22-OCT-1998; 98US-0177315.

PA (UNITM) UNIV WASHINGTON.

PI Johnson EM, Easton R;

PT WPI; 2000-339513/29.

PS Claim 4; Page 33; 43pp; English.

XX The present sequence is a specifically claimed truncated BAX protein
CC tBAX78 which inhibits neuronal apoptosis induced by trophic factor
CC deprivation. The protein consists of first 78 amino acids of human
CC BAX alpha, that includes the N-terminal region and BH3
CC domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of
CC the full-length BAX alpha. The tBAX protein lacking only the
CC transmembrane domain has been shown to have anti-apoptotic activity.
CC The present sequence is used to treat diseases associated with neuronal
CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
CC spinal cord injury, head trauma and stroke.

XX Sequence 78 AA;

Query Match 100.0%; Score 20; DB 21; Length 78;

Best Local Similarity 100.0%; Pred. No. 5.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGCGPTSSEQIM 20
|||||

1

DB 1 MDGSGEOPRGCGPTSSEQIM 20

RESULT 5
AAV70822
ID AAV70822 standard; Protein; 78 AA.

AC AAV70822;

DT 31-JUL-2000 (first entry)

DE Human neuroprotective truncated BAX protein tBAX78 mutant.

KW Human; truncated BAX protein; tBAX78M; BAX alpha; BCL-2 family; mutant;

KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;

KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;

KW spinal cord injury; head trauma; stroke.

OS Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 55 /note= "Wild type Ser is substituted by Ala"

FT Misc-difference 60 /note= "Wild type Ser is substituted by Ala"

FT Region 71..78 /note= "sequence not found in BAX alpha"

WO200023083-A1.

PD 27-APR-2000.

PF 22-OCT-1999; 99WO-US24747.

PR 22-OCT-1998; 98US-0177315.

PA (UNITM) UNIV WASHINGTON.

PI Johnson EM, Easton R;

PT WPI; 2000-339513/29.

PS N-PSDB; AAD00125.

PS Claim 4; Page 34; 43pp; English.

XX The present sequence is a specifically claimed truncated BAX protein,
CC tBAX78 mutant (tBAX78M) which inhibits neuronal apoptosis induced by
CC trophic factor deprivation. The protein consists of the N-terminal
CC region and a portion of BH3 domain of human BAX alpha, and a novel
CC C-terminal sequence of 8 amino acids not present in BAX alpha.
CC It lacks the BH1, BH2 and C-terminal transmembrane
CC domains of the full-length BAX alpha. The tBAX protein lacking only the
CC transmembrane domain has been shown to have anti-apoptotic activity.
CC The present sequence is used to treat diseases associated with neuronal
CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
CC spinal cord injury, head trauma and stroke.

XX Sequence 78 AA;

Query Match 100.0%; Score 20; DB 21; Length 78;

Best Local Similarity 100.0%; Pred. No. 5.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGCGPTSSEQIM 20
|||||

DB 1 MDGSGEOPRGCGPTSSEQIM 20
|||||

RESULT 6

AAV34149
 ID AAV34149 standard; Protein; 131 AA.
 XX
 AC AAV34149;
 XX
 DT 30-NOV-1999 (first entry)
 XX
 DE Human truncated Bax protein.
 XX
 KM Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 59..101
 FT /note="Portion of BH3 domain essential for dimerisation"
 XX
 PN W09946371-A2.
 XX
 PD 16-SEP-1999.
 XX
 PF 11-MAR-1999; 99WO-US05359.
 XX
 PR 11-MAR-1998; 98US-0077541.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI McDonnell TJ, Swisher SG, Fang B, Bruckheimer EM, Sarkiss MG;
 PI Ji L, Roth JA.
 XX
 DR WPI; 1999-551404/46.
 DR N-PSDB; AA219763.
 XX
 PT New adenovirus vectors, used for killing or inhibiting the growth of
 PT cells and for treating cancers -
 XX
 PS Claim 26: Page 148-149; 151pp; English.
 XX
 CC This sequence represents a human truncated Bax protein. The cDNA
 CC contains a single base deletion relative to the wild-type (AA219764),
 CC causing a frameshift which leads to translation of a premature stop
 CC codon, resulting in a truncated protein. However, the domain responsible
 CC for its function is still present in the truncated protein. Bax (Bcl-2
 CC associated X protein) is a proapoptotic member of the Bcl-2 gene family.
 CC Bax functions as a primary response gene in the p53-regulated apoptotic
 CC pathway. The Bax gene promoter has 4 p53 binding sites and the
 CC expression of Bax is upregulated at the transcriptional level by p53, and
 CC Bax mRNA and protein expression have been shown to increase following
 CC induction of p53. Bax protein can function as a homodimer, or it can
 CC heterodimerise with other Bcl-2 gene family members such as the
 CC antiapoptotic protein Bcl-2. Heterodimerisation of Bcl-2 family members
 CC provides a means of controlling cell death via the "rheostat" model. This
 CC model suggests that the relative amounts of Bcl-2 and Bax determine the
 CC susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess,
 CC Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is
 CC in excess, however, Bax homodimers predominate and the cell becomes
 CC susceptible to apoptosis following exposure to an apoptotic stimulus.
 CC Additionally, Bax can function in its monomeric form to accelerate cell
 CC death. Use of novel adenoviral vectors containing this Bax gene may
 CC augment and complement wild-type p53 gene therapy, which induces a G1
 CC cell cycle arrest and/or apoptosis in malignant cells carrying p53
 CC mutations. In addition, Bax overexpression could provide the apoptotic
 CC effect of p53 without the need for p53 itself.
 CC
 SQ Sequence 131 AA:

Query Match 100.0%; Score 20; DB 20; Length 131;
 Best Local Similarity 100.0%; Pred. No. 9.1e-12;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEPGPGGPTSSQIM 20
 Db 1 MDGSGEPGPGGPTSSQIM 20

RESULT 7
 ID AAR71406
 XX AAR71406 standard; Protein; 192 AA.
 AC AAR71406;
 XX
 DT 15-NOV-1995 (first entry)
 XX
 DE Human Bax protein.
 XX
 KM Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line;
 KM apoptosis; membrane-associated cytoplasmic protein; B cell; T cell;
 KM proliferation; cell cycle progression; Bax; apoptotic cell death;
 KM apoptosis; cytokine; death repressor; BH1; BH2; cancer therapy;
 KM hyperplasia; immunodeficiency disease; AIDS; neurodegeneration;
 KM ischaemic cell death.
 XX
 OS Homo sapiens.
 XX
 PN W09505750-A.
 XX
 PD 02-MAR-1995.
 XX
 PF 24-AUG-1994; 94WO-US09701.
 XX
 PR 26-AUG-1993; 93US-0112208.
 PR 25-MAY-1994; 94US-0248819.
 XX
 PA (UNITW) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ;
 PI WPI; 1995-106605/14.
 DR N-PSDB; AAQ97606.
 XX
 PT Methods for producing and identifying mutant bcl-2 proteins -
 PT that lack death repressor activity and/or lacks binding to Bax.
 XX
 PS Disclosure; Fig 3; 133pp; English.
 XX
 CC This sequence represents human Bax protein. Bax is a protein which is
 CC associated with the human bcl-2 alpha and beta proteins, the sequences
 CC of which are given in AAR71404-05 respectively. bcl-2 is encoded by a
 CC proto-oncogene and is capable of inhibiting apoptosis in many
 CC hematopoietic cell systems. bcl-2 is a 26 kD membrane-associated
 CC cytoplasmic protein and is thought to function by enhancing the survival
 CC of hematopoietic cells of B and T origins rather than directly promoting
 CC proliferation of these cell types. bcl-2 has not been shown to directly
 CC promote cell cycle progression nor does it necessarily alter the dose
 CC response to limiting concentrations of IL-3. bcl-2 has been shown to
 CC form heterodimers with this 21 kD protein, Bax. Overexpressed Bax
 CC accelerates apoptotic cell death induced by cytokine deprivation in an
 CC IL-3 dependent cell line, and it also acts to counter the death repressor
 CC activity of bcl-2. Therefore, the ratio between bcl-2 and Bax determines
 CC cell survival or death following an apoptotic stimulus. The invention
 CC gives a mutant form of bcl-2 in which there is at least one amino acid
 CC substitution or deletion in the BH1 or BH2 domains. This makes the
 CC mutant protein substantially incapable of binding Bax and/or incapable
 CC of death repressor activity. Down regulation of bcl-2 is useful in
 CC cancer therapy, controlling hyperplasias and eliminating self-reactive
 CC clones in autoimmunity by favouring death effector molecules. Up
 CC regulating bcl-2 is beneficial in treatment and diagnosis of immuno-
 CC deficiency diseases, including AIDS and neurodegenerative and ischemic
 CC cell death.
 CC
 SQ Sequence 192 AA:

Query Match 100.0%; Score 20; DB 16; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDSCGEOPRGCGPTSSEQIM 20
|||||
Db 1 MDSCGEOPRGCGPTSSEQIM 20

RESULT 8
AAV34150

ID AAV34150 standard; Protein; 192 AA.

XX AAV34150;

DT 30-NOV-1999 (first entry)

DE Human wild-type Bax protein.

KM Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Domain 59..101 /note="Portion of BH3 domain essential for dimerisation"

PN WO946371-A2.

PD 16-SEP-1999.

PF 11-MAR-1999; 99WO-US053359.

PR 11-MAR-1998; 98US-0077541.

PA (TEXA) UNIV TEXAS SYSTEM.

PI McDonnell TJ, Swisher SG, Fang B, Bruckheimer EM, Sarkiss MC;

PT Ji L, Roth JA;

DR WPI; 1999-551404/46.

DR N-PSDB; AA219764.

PT New adenovirus vectors, used for killing or inhibiting the growth of
cells and for treating cancers .

XX Disclosure; Page 149-150; 151pp; English.

CC This sequence represents human wild-type Bax protein. A naturally
CC occurring mutant protein (AAV34149) was also isolated. Bax (Bcl-2
CC associated X protein) is a proapoptotic member of the Bcl-2 gene family.
CC Bax functions as a primary response gene in the p53-regulated apoptotic
CC pathway. The Bax gene promoter has 4 p53 binding sites and the
CC expression of Bax is upregulated at the transcriptional level by p53, and
CC Bax mRNA and protein expression have been shown to increase following
CC induction of p53. Bax protein can function as a homodimer, or it can
CC heterodimerise with other Bcl-2 gene family members such as the
CC antiapoptotic protein Bcl-2. Heterodimerisation of Bcl-2 family members
CC provides a means of controlling cell death via the "rheostat" model. This
CC model suggests that the relative amounts of Bcl-2 and Bax determine the
CC susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess,
CC Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is
CC in excess, however, Bax homodimers predominate and the cell becomes
CC susceptible to apoptosis following exposure to an apoptotic stimulus.
CC Additionally, Bax can function in its monomeric form to accelerate cell
CC death. Use of novel adenoviral vectors containing the Bax gene may
CC augment and complement wild-type p53 gene therapy, which induces a G1
CC cell cycle arrest and/or apoptosis in malignant cells carrying p53
CC mutations. In addition, Bax overexpression could provide the apoptotic
CC effect of p53 without the need for p53 itself.

XX Sequence 192 AA;

Query Match 100.0%; Score 20; DB 20; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDSCGEOPRGCGPTSSEQIM 20
|||||
Db 1 MDSCGEOPRGCGPTSSEQIM 20

RESULT 9
AAV05435

ID AAV05435 standard; peptide; 192 AA.

XX AAV05435;

DT 02-JUL-1999 (first entry)

DE Human BAX protein sequence.

XX BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;
KW apoptosis promoter; cancer cell; virus infected cell; inflammation;
KW autoantibody producing cell; cancer; Lymphoproliferative condition;
KW arthritis; autoimmune disease; therapy.

OS Homo sapiens.

PN WO9916787-A1.

PD 08-APR-1999.

PF 22-SEP-1998; 98WO-US19765.

PR 07-OCT-1997; 97US-0946039.

PR 26-SEP-1997; 97US-0060133.

PA (UNIM) UNIV WASHINGTON.

PI Korsmeyer SJ;

DR WPI; 1999-255058/21.

PT Bcl homology domain 3 polypeptide

PS Disclosure; Fig 21c; 104pp; English.

CC This sequence represents the human BAX protein.
CC The invention relates to a bcl homology domain 3 (BH3 domain),
CC derived from a proapoptotic member of the Bcl-2 family. The
CC BH3 polypeptide can be used in a method for promoting apoptosis in a
CC target cell, especially where the cell is a cancer cell a virus infected
CC cell or an autoantibody producing cell. The BH3 polypeptide can be used
CC in therapeutic compositions for treating disease including cancer, other
CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
CC diseases, which may result from the down regulation of cell death
CC regulation.

XX Sequence 192 AA;

Query Match 100.0%; Score 20; DB 20; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDSCGEOPRGCGPTSSEQIM 20
|||||
Db 1 MDSCGEOPRGCGPTSSEQIM 20

RESULT 10

AAW87804

ID AAW87804 standard; Protein; 192 AA.

XX AAW87804;

DT 10-MAR-1999 (first entry)

DE A human Bcl-2 associated protein designated Bax.

XX

```

KM Human: Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;
KW bcl-2-related function; apoptosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 97..118 /note="B1 domain"
FT 146..168
FT Domain /note="BH2 domain"
XX
XX
PN US5856171-A.
XX
PD 05-JAN-1999.
XX
PF 10-NOV-1994; 94US-0337646.
XX
PR 10-NOV-1994; 94US-0337646.
PR 26-AUG-1993; 93US-0112208.
PR 25-MAY-1994; 94US-0248819.
XX
XX (UNIT ) UNIV WASHINGTON.
XX
PI Korsmeyer SJ;
XX
DR WPI: 1999-105119/09.
DR N-PSDB: AAV84005.
XX
XX
PT DNA composition encoding bcl-2 two-hybrid and reporter system - for
PT identifying modulators of bcl-2 function
XX
XX Example 1; Columns 71-74; 105pp; English.
XX
XX The present sequence represents a human Bcl-2 associated protein
XX designated Bax. The Bax protein is used in a composition which
XX comprises a bcl-2 family member polypeptide, a naturally occurring
XX Bax polypeptide and an antibody that binds to the Bax polypeptide.
XX The composition is used to identify modulators of bcl-2-related
XX function, e.g. substances that inhibit binding of Bax to bcl-2,
XX which would be potentially useful as drugs for modulating
XX apoptosis.
XX
SQ Sequence 192 AA:

```

```

Query Match 100.0%; Score 20; DB 20; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDGSGEQPRGCGPTSSSEQIM 20
Db 1 MDGSGEQPRGCGPTSSSEQIM 20

```

```

RESULT 11
AAW87809
ID AAW87809 standard; Protein: 192 AA.
XX
XX AAW87809;
AC
XX
DT 10-MAR-1999 (first entry)
XX
DE A human Bcl-2 associated protein designated Bax.
XX
XX Human: Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;
KW bcl-2-related function; apoptosis.
XX
XX Homo sapiens.
XX
XX US5856171-A.
XX
XX 05-JAN-1999.
XX
XX 10-NOV-1994; 94US-0337646.

```

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XX
XX 10-NOV-1994; 94US-0337646.
PR 26-AUG-1993; 93US-0112208.
PR 25-MAY-1994; 94US-0248819.
XX
XX (UNIT ) UNIV WASHINGTON.
XX
XX Korsmeyer SJ;
XX
XX WPI: 1999-105119/09.
XX
XX
PT DNA composition encoding bcl-2 two-hybrid and reporter system - for
PT identifying modulators of bcl-2 function
XX
XX Example 7; Fig 7; 105pp; English.
XX
XX The present sequence represents a human Bcl-2 associated protein
XX designated Bax. The Bax protein is used in a composition which
XX comprises a bcl-2 family member polypeptide, a naturally occurring
XX Bax polypeptide and an antibody that binds to the Bax polypeptide.
XX The composition is used to identify modulators of bcl-2-related
XX function, e.g. substances that inhibit binding of Bax to bcl-2,
XX which would be potentially useful as drugs for modulating
XX apoptosis.
XX
SQ Sequence 192 AA:

```

```

Query Match 100.0%; Score 20; DB 20; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDGSGEQPRGCGPTSSSEQIM 20
Db 1 MDGSGEQPRGCGPTSSSEQIM 20

```

```

RESULT 12
AAW70827
ID AAW70827 standard; Protein: 192 AA.
XX
XX AAW70827;
AC
XX
DT 31-JUL-2000 (first entry)
XX
DE Human BAX alpha protein.
XX
XX Human BAX alpha protein.
KW Human: truncated BAX protein; tBAX; BAX alpha; BCL-2 family; head trauma;
KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
KW spinal cord injury; stroke; pro-apoptotic; PCD; programmed cell death.
XX
XX Homo sapiens.
XX
XX

```

```

FH Key Location/Qualifiers
FT Region 1..58
FT /label= N-terminal_region
FT Domain 59..73
FT /label= BH3_domain
FT Domain 98..118 /note="BCL-2 Homology domain 3"
FT /label= BH1_domain
FT Domain 150..165
FT /label= BH2_domain
FT Domain 169..188 /label= Transmembrane_domain
XX
XX WO200023083-A1.
XX
XX 27-APR-2000.
XX
XX 22-OCT-1999; 99WO-US24747.
XX
XX 22-OCT-1996; 98US-0177315.

```

```
XX (UNIM ) UNIV WASHINGTON.
PA
XX Johnson EM, Easton R;
PI
XX WPI: 2000-339513/29.
DR
XX Truncated BAX polypeptides useful for preventing apoptosis of neurons
PT for the treatment of nervous system disorders -
XX
XX Disclosure: Page 35-36; 43pp; English.
PS
XX The present sequence is a human BAX alpha protein, a pro-apoptotic
CC protein which is a member of BCL-2 family of proteins that are involved
CC in regulation of neuronal programmed cell death. The patent discloses
CC specific truncated proteins derived from BAX alpha which inhibit neuronal
CC apoptosis induced by trophic factor deprivation. The anti-apoptotic
CC truncated BAX (tBAX) proteins include tBAX70, tBAX78 and their mutants.
CC These proteins contain the N-terminal region and at least a portion of
CC the BH3 domain of BAX alpha and lack the BH1, BH2 and C-terminal
CC transmembrane domains. The tBAX protein lacking only the
CC transmembrane domain has been shown to have anti-apoptotic activity.
CC The tBAX proteins are used to treat diseases associated with neuronal
CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
CC spinal cord injury, head trauma and stroke.
XX
XX Sequence 192 AA:
SQ
XX
XX Query Match 100.0%; Score 20; DB 21; Length 192;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-11;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGGPTSSQIM 20
Db 1 MDGSGEOPRGGPTSSQIM 20

RESULT 13
AAY69202
ID AAY69202 standard; peptide: 192 AA.
XX
XX AAY69202:
AC
XX
XX 30-MAY-2000 (first entry)
DT
XX
XX Amino acid sequence of the human Bax protein.
DE
XX
XX Pro-apoptotic peptide; Bax; BH3 domain; channel inducer; transport;
KM cytochrome C transport; mitochondria; apoptosis; ion selectivity;
KM anti-apoptotic BCL-2 family member; neoplasia; Epstein Barr virus;
KM African swine fever virus; adenovirus; lymphoproliferative condition;
KM cancer; arthritis; Crohn's disease; inflammation; autoimmune disease;
KM immunodeficiency; senescence; neurodegenerative disease;
KM reperfusion cell death; infertility; wound.
XX
XX Homo sapiens.
OS
XX
XX WO200006187-A2.
PN
XX
XX 10-FEB-2000.
PD
XX
XX 30-JUL-1999; 99WO-US17276.
PF
XX
XX 31-JUL-1998; 98US-0127048.
PR
XX
XX (UNIM ) UNIV WASHINGTON.
PA
XX
XX Korsmeyer SJ, Schlesinger PH;
PI
XX
XX WPI: 2000-195193/17.
DR
XX
XX Modulating apoptosis in cells by modulating channel ion selectivity for
PT transport of cytochrome C -
```

```
XX Disclosure: Page 34; 57pp; English.
PS
XX The present sequence represents the Bax protein. A pro-apoptotic
CC peptide can be derived from the BH3 domain. The peptide is an inducer
CC of formation of a channel for transport of cytochrome C out of
CC mitochondria. The peptide induces apoptosis in a cell. The peptide
CC changes the ion selectivity of an anti-apoptotic BCL-2 family member
CC from potassium selective to chloride selective. The specification
CC also describes inhibitors of apoptosis in cells. The inhibitors and
CC inducers can be used to treat patients, preferably humans with a
CC condition mediated by excessive down-regulation of apoptosis,
CC especially conditions chosen from neoplasias, diseases caused by
CC Epstein Barr virus, African swine fever virus and adenovirus,
CC lymphoproliferative conditions, cancer, arthritis, Crohn's disease,
CC inflammation and autoimmune disease or a condition mediated by
CC excessive apoptosis, especially immunodeficiency diseases, senescence,
CC neurodegenerative disease, ischemic and reperfusion cell death,
CC infertility and wounds. The methods can also be used to identify
CC apoptosis-modulating compounds.
XX
XX Sequence 192 AA:
SQ
XX
XX Query Match 100.0%; Score 20; DB 21; Length 192;
XX Best Local Similarity 100.0%; Pred. No. 1.3e-11;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGGPTSSQIM 20
Db 1 MDGSGEOPRGGPTSSQIM 20

RESULT 14
AAB74121
ID AAB74121 standard; Protein; 192 AA.
XX
XX AAB74121:
AC
XX
XX 22-MAY-2001 (first entry)
DT
XX
XX Human bcl-2 associated X protein (Bax) #1.
DE
XX
XX Human; Bax; cytosolic; immunosuppressive; immunostimulant; infection;
KM apoptosis modulator; bcl-2 associated X protein; cancer therapy; AIDS;
KM autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;
KM myocardial infarction; traumatic brain injury; ischemia;
KM neurodegenerative diseases; hepatitis; transplant rejection; toxemia;
KM lymphoproliferative disease.
XX
XX Homo sapiens.
OS
XX
XX US6184202-B1.
PN
XX
XX 06-FEB-2001.
PD
XX
XX 11-SEP-1997; 97US-0927326.
PF
XX
XX 10-NOV-1994; 94US-0337646.
PR
XX
XX 26-AUG-1993; 93US-0112208.
PR
XX
XX 25-MAY-1994; 94US-0248819.
XX
XX (UNIM ) UNIV WASHINGTON.
PA
XX
XX Korsmeyer SJ;
PI
XX
XX WPI: 2001-256104/26.
DR
XX
XX N-PSDB; AAF77704.
DR
XX
XX Modulating apoptosis of a cell, useful in maintaining homeostasis in
PT adult tissues, or treating proliferative or autoimmune diseases,
PT comprises administering a bcl-2 polypeptide that interacts with a 21 kd
PT bcl-2 associated X protein -
```

PS Claim 3; Fig 3; 105pp; English.
 XX
 CC The present invention relates to a method of modulating apoptosis of a
 CC cell. The method comprises administering to the cell an agent
 CC comprising a BH1 domain or BH2 domain, capable of modulating formation of
 CC at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL
 CC complexes, bcl-2 associated X protein (Bax):Bax complexes, bcl-2:Bax
 CC complexes or bcl-XL:Bax complexes. Modulating apoptosis is especially
 CC useful in cancer therapy, and treating autoimmunity, immunodeficiency
 CC diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke,
 CC traumatic brain injury, neurodegenerative diseases, aging, ischemia,
 CC toxemia, infection, hepatitis, transplant rejection, and
 CC lymphoproliferative diseases. The present sequence is human Bax, which
 CC was used in the method of the present invention.
 XX
 SQ Sequence 192 AA;
 Query Match 100.0%; Score 20; DB 22; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDGSGEQPRGGPTSSQIM 20
 Db 1 MDGSGEQPRGGPTSSQIM 20
 RESULT 15
 AAB74126
 ID AAB74126 standard; Protein: 192 AA.
 XX
 AC AAB74126;
 XX
 DT 22-MAY-2001 (first entry)
 XX
 DE Human bcl-2 associated X protein (bax) #2.
 XX
 KM Human; Bax: cytostatic; immunosuppressive; immunostimulant; infection;
 KM apoptosis modulator; bcl-2 associated X protein; cancer therapy; AIDS;
 KM autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;
 KM myocardial infarction; traumatic brain injury; ischemia;
 KM neurodegenerative diseases; hepatitis; transplant rejection; toxemia;
 KM lymphoproliferative disease.
 XX
 OS Homo sapiens.
 XX
 PN US6184202-B1.
 XX
 PD 06-FEB-2001.
 XX
 PF 11-SEP-1997; 97US-0927326.
 XX
 PR 10-NOV-1994; 94US-0337646.
 PR 26-AUG-1993; 93US-0112208.
 PR 25-MAY-1994; 94US-0248819.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ;
 XX
 DR WPI; 2001-256104/26.
 XX
 XX
 PT Modulating apoptosis of a cell, useful in maintaining homeostasis in
 PT adult tissues, or treating proliferative or autoimmune diseases,
 PT comprises administering a bcl-2 polypeptide that interacts with a 21 kD
 PT bcl-2 associated X protein -
 XX
 XX Example 7; Fig 7; 105pp; English.
 XX
 CC The present invention relates to a method of modulating apoptosis of a
 CC cell. The method comprises administering to the cell an agent,
 CC comprising a BH1 domain or BH2 domain, capable of modulating formation of
 CC at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL
 CC complexes, bcl-2 associated X protein (Bax):Bax complexes, bcl-2:Bax

CC complexes or bcl-XL:Bax complexes. Modulating apoptosis is especially
 CC useful in cancer therapy, and treating autoimmunity, immunodeficiency
 CC diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke,
 CC traumatic brain injury, neurodegenerative diseases, aging, ischemia,
 CC toxemia, infection, hepatitis, transplant rejection, and
 CC lymphoproliferative diseases. The present sequence is human Bax, which
 CC was used in a sequence alignment in the present invention, with murine
 CC Bax (AAB74125), human Bcl-2 (AAB74127) and murine Bcl-2 (AAB74128).
 XX
 SQ Sequence 192 AA;
 Query Match 100.0%; Score 20; DB 22; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 MDGSGEQPRGGPTSSQIM 20
 Search completed: January 7, 2003, 12:38:30
 Job time : 31.7949 secs

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REFERENCE/DOCKET NUMBER: 976175
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..192
OTHER INFORMATION: /note="Murine BAX polypeptide"
US-08-856-034-3

Query Match      88.5%; Score 69; DB 2; Length 192;
Best Local Similarity 73.7%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDSCGXXXXXGGPTSSQI 19
Db 1 MDSCGEQLGSGGPTSSQI 19

RESULT 11
US-08-856-034-8
Sequence 8, Application US/08856034
Patent No. 5955595
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856.034
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, Donald R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976175
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..192
OTHER INFORMATION: /note="Murine BAX polypeptide"
US-08-856-034-8

Query Match      88.5%; Score 69; DB 2; Length 192;
Best Local Similarity 73.7%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDSCGXXXXXGGPTSSQI 19
Db 1 MDSCGEQLGSGGPTSSQI 19

RESULT 12
US-09-127-048-6
Sequence 6, Application US/09127048
Patent No. 6165732
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
APPLICANT: Schlesinger, Paul H.
TITLE OF INVENTION: Method for Identifying Apoptosis Modulating Compounds
FILE REFERENCE: 6029-6052
CURRENT APPLICATION NUMBER: US/09/127,048
CURRENT FILING DATE: 1998-07-31
EARLIER APPLICATION NUMBER: 60/061,823
EARLIER FILING DATE: 1997-10-14
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 192
TYPE: PRT
ORGANISM: Mouse
US-09-127-048-6

Query Match      88.5%; Score 69; DB 4; Length 192;
Best Local Similarity 73.7%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDSCGXXXXXGGPTSSQI 19
Db 1 MDSCGEQLGSGGPTSSQI 19

RESULT 13
US-08-927-326-3
Sequence 3, Application US/08927326
Patent No. 6184202
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,326
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,646
FILING DATE: 10-NOV-1994
APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000620
TELECOMMUNICATION INFORMATION:

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TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..192
OTHER INFORMATION: /note="Protein sequence of murine
OTHER INFORMATION: Bax."
US-08-927-326-3

Query Match 88.5%; Score 69; DB 4; Length 192;
Best Local Similarity 73.7%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDGSGXXXXXGGPTSSFOI 19
||||| |||||||
DB 1 MDGSGEQLGSGGPTSSFOI 19

RESULT 14
US-08-927-326-8
Sequence 8, Application US/08927326
Patent No. 6184202
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Knourle and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,326
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,646
FILING DATE: 10-NOV-1994
APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-927-326-8

Query Match 88.5%; Score 69; DB 4; Length 192;
Best Local Similarity 73.7%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDGSGXXXXXGGPTSSFOI 19
||||| |||||||
DB 1 MDGSGEQLGSGGPTSSFOI 19

RESULT 15
US-09-166-028-1
Sequence 1, Application US/09166028
Patent No. 6245885
GENERAL INFORMATION:
APPLICANT: Gordon C. Shore et al.
TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
FILE REFERENCE: 50013/011001
CURRENT APPLICATION NUMBER: US/09/166,028
CURRENT FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic based on consensus sequence of Homo
OTHER INFORMATION: sapiens, Mus musculus, and Rattus norvegicus
NAME/KEY: VARIANT
LOCATION: (6)...(10)
OTHER INFORMATION: Xaa at 6 can be E or D; Xaa at 7 can be Q or H;
OTHER INFORMATION: Xaa at 8 can be L or P; Xaa at 9 can be R or G;
OTHER INFORMATION: Xaa at 10 can be S or G;
US-09-166-028-1

Query Match 87.2%; Score 68; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MDGSGXXXXXGGPTSSFOI 19

Search completed: January 7, 2003, 12:31:49
Job time: 12.2051 secs

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: IAS MBP 90-101
; OTHER INFORMATION: CH1.H.CH2 recombinant MHC class II-peptide-Ig
; OTHER INFORMATION: fusion complex
US-09-815-837-70
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Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
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      111      11:111
Db      243 GSGGGGGGGGSSSE 257
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RESULT 14
US-09-815-837-69
; Sequence 69, Application US/09815837
; Patent No. US2002008241A1
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```
; GENERAL INFORMATION:
```

```
; APPLICANT: Carter, Darrick
```

```
; APPLICANT: Zhu, Shirley
```

```
; APPLICANT: Arimilli, Subhashini
```

```
; APPLICANT: Wang, Aijun
```

```
; APPLICANT: Corixa Corporation
```

```
; TITLE OF INVENTION: Immune Mediators and Related Methods
```

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; FILE REFERENCE: 014058-005670US
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; CURRENT APPLICATION NUMBER: US/09/815,837
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; PRIOR FILING DATE: 2001-03-22
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; PRIOR APPLICATION NUMBER: US 60/191,274
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; PRIOR FILING DATE: 2000-03-22
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; PRIOR APPLICATION NUMBER: US 60/204,249
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; PRIOR FILING DATE: 2000-05-15
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; PRIOR APPLICATION NUMBER: US 60/264,003
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; PRIOR FILING DATE: 2001-01-23
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; NUMBER OF SEQ ID NOS: 129
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; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 69
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; LENGTH: 676
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; TYPE: PRT
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; ORGANISM: Artificial Sequence
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; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: IAS MBP 1-14
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```
; OTHER INFORMATION: CH1.H recombinant MHC class II-peptide-Ig fusion
```

```
; OTHER INFORMATION: complex
```

```
US-09-815-837-69
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Query Match          46.2% Score 36; DB 10; Length 676;
Best Local Similarity 53.3%; Pred. No. 97;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
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```
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US-09-815-837-68
; Sequence 68, Application US/09815837
; Patent No. US2002008241A1
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; GENERAL INFORMATION:
```

```
; APPLICANT: Carter, Darrick
```

```
; APPLICANT: Zhu, Shirley
```

```
; APPLICANT: Arimilli, Subhashini
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; APPLICANT: Wang, Aijun
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; APPLICANT: Corixa Corporation
```

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; TITLE OF INVENTION: Immune Mediators and Related Methods
```

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; FILE REFERENCE: 014058-005670US
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; CURRENT APPLICATION NUMBER: US/09/815,837
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; PRIOR FILING DATE: 2001-03-22
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; PRIOR APPLICATION NUMBER: US 60/191,274
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; PRIOR FILING DATE: 2000-03-22
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; PRIOR APPLICATION NUMBER: US 60/204,249
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/264,003
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 68
; LENGTH: 678
; TYPE: PRT
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; ORGANISM: Artificial Sequence
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; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: IAS MBP 1-14
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; OTHER INFORMATION: CH1.H.CH2.CH3 recombinant MHC class II-peptide-Ig
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; OTHER INFORMATION: fusion complex
```

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US-09-815-837-68
Query Match          46.2% Score 36; DB 10; Length 678;
Best Local Similarity 53.3%; Pred. No. 98;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
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Db      243 GSGGGGGGGGSSSE 257
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:28:23 : Search time 11.2051 Seconds
(without alignments)
49.891 Million cell updates/sec

Title: US-09-876-204-1
Perfect score: 78
Sequence: 1 MDGSGXXXXGPTSSSEQI 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents-AA: *
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4: /cgn2.6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2.6/ptodata/1/1aa/PC105.COMB.pep: *
6: /cgn2.6/ptodata/1/1aa/backfill1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	69	88.5	20	4	US-09-166-028-4
2	69	88.5	192	1	US-08-112-208C-3
3	69	88.5	192	1	US-08-112-208C-8
4	69	88.5	192	1	US-08-248-819A-3
5	69	88.5	192	1	US-08-248-819A-8
6	69	88.5	192	2	US-08-337-646A-3
7	69	88.5	192	2	US-08-337-646A-8
8	69	88.5	192	2	US-08-856-531-3
9	69	88.5	192	2	US-08-856-531-8
10	69	88.5	192	2	US-08-856-034-3
11	69	88.5	192	2	US-08-856-034-8
12	69	88.5	192	4	US-09-127-048-6
13	69	88.5	192	4	US-08-927-326-3
14	69	88.5	192	4	US-08-927-326-8
15	68	87.2	19	4	US-09-166-028-1
16	68	87.2	20	4	US-09-166-028-5
17	67	85.9	20	4	US-09-166-028-3
18	67	85.9	192	1	US-08-112-208C-2
19	67	85.9	192	1	US-08-112-208C-9
20	67	85.9	192	1	US-08-248-819A-2
21	67	85.9	192	1	US-08-248-819A-9
22	67	85.9	192	1	US-08-607-269-25
23	67	85.9	192	1	US-08-471-058-13
24	67	85.9	192	2	US-08-337-646A-2
25	67	85.9	192	2	US-08-337-646A-9
26	67	85.9	192	2	US-08-856-531-2
27	67	85.9	192	2	US-08-856-531-9

28	67	85.9	192	2	US-08-856-034-2	Sequence 2, Appli
29	67	85.9	192	2	US-08-856-034-9	Sequence 9, Appli
30	67	85.9	192	3	US-08-471-057-13	Sequence 13, Appli
31	67	85.9	192	4	US-09-127-048-7	Sequence 7, Appli
32	67	85.9	192	4	US-08-927-326-2	Sequence 2, Appli
33	67	85.9	192	4	US-08-927-326-9	Sequence 9, Appli
34	67	85.9	192	5	PCP-US95-04600-25	Sequence 25, Appli
35	67	85.9	221	1	US-08-616-732A-9	Sequence 9, Appli
36	67	85.9	221	4	US-09-037-742B-9	Sequence 9, Appli
37	46	59.0	25	1	US-08-798-897-21	Sequence 21, Appli
38	46	59.0	25	2	US-08-978-523-21	Sequence 21, Appli
39	40	51.3	481	3	US-09-330-095-1	Sequence 1, Appli
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41	38	48.7	154	4	US-09-397-787-16	Sequence 16, Appli
42	38	48.7	473	2	US-08-249-189-16	Sequence 16, Appli
43	38	48.7	473	2	US-08-484-624A-16	Sequence 16, Appli
44	38	48.7	473	2	US-08-477-733B-16	Sequence 16, Appli
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ALIGNMENTS

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RESULT 1
US-09-166-028-4
: Sequence 4, Application US/09166028
: Patent No. 6245885
: GENERAL INFORMATION:
: APPLICANT: Gordon C. Shore et al.
: TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
: FILE OF INVENTION: REAGENTS AND METHODS
: CURRENT REFERENCE: 50013/011001
: CURRENT APPLICATION NUMBER: US/09/166,028
: CURRENT FILING DATE: 1998-10-05
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-166-028-4

Query Match      88.5%: Score 69: DB 4: Length 20:
Best Local Similarity 73.7%: Pred. NO. 2.8e-06:
Matches 14: Conservative 0: Mismatches 5: Indels 0:

QY      1 MDGSGXXXXGPTSSSEQI 19
      ||||| |||||
DB      1 MDGSGQLGSGGPTSSSEQI 19

RESULT 2
US-08-112-208C-3
: Sequence 3, Application US/08112208C
: Patent No. 5691179
: GENERAL INFORMATION:
: APPLICANT: KORSMEYER, Stanley J.
: TITLE OF INVENTION: CELL DEATH REGULATORS
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESS: Townsend and Townsend Khourie and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/112,208C

```

FILING DATE: 26-AUG-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..192
OTHER INFORMATION: /note="Protein sequence of murine
OTHER INFORMATION: Bax."

US-08-112-208C-3

Query Match 88.5%; Score 69; DB 1; Length 192;
Best Local Similarity 73.7%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDGSGXXXXGGPTSSDOI 19
Db 1 MDGSGEQLGSGGPTSSDOI 19

RESULT 3
US-08-112-208C-8
Sequence 8, Application US/08112208C
Patent No. 5691179
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/112,208C
FILING DATE: 26-AUG-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-112-208C-8

Query Match 88.5%; Score 69; DB 1; Length 192;

Best Local Similarity 73.7%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDGSGXXXXGGPTSSDOI 19
Db 1 MDGSGEQLGSGGPTSSDOI 19

RESULT 4
US-08-248-819A-3
Sequence 3, Application US/08248819A
Patent No. 5700638
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,819A
FILING DATE: 25-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..192
OTHER INFORMATION: /note="Protein sequence of murine
OTHER INFORMATION: Bax."

US-08-248-819A-3

Query Match 88.5%; Score 69; DB 1; Length 192;
Best Local Similarity 73.7%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDGSGXXXXGGPTSSDOI 19
Db 1 MDGSGEQLGSGGPTSSDOI 19

RESULT 5
US-08-248-819A-8
Sequence 8, Application US/08248819A
Patent No. 5700638
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 60

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CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Hourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,819A
FILING DATE: 25-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-248-819A-8

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Query Match      88.5%: Score 69; DB 1; Length 192;
Best Local Similarity 73.7%: Pred. No. 3.2e-05;
Matches 14: Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 1 MDGSGXXXXGPTSEQI 19
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Db 1 MDGSGEQLGSGPTSEQI 19

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RESULT 6
US-08-337-646A-3
Sequence 3, Application US/08337646A
Patent No. 5856171
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Hourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,646A
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208

```

```

FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..192
OTHER INFORMATION:
OTHER INFORMATION: Bax." "Protein sequence of murine
US-08-337-646A-3

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Query Match      88.5%: Score 69; DB 2; Length 192;
Best Local Similarity 73.7%: Pred. No. 3.2e-05;
Matches 14: Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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```

QY 1 MDGSGXXXXGPTSEQI 19
    ||||| |||||
Db 1 MDGSGEQLGSGPTSEQI 19

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```

RESULT 7
US-08-337-646A-8
Sequence 8, Application US/08337646A
Patent No. 5856171
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Hourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,646A
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,819
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000620
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single

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TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-337-646A-8

Query Match 88.5%; Score 69; DB 2; Length 192;
Best Local Similarity 73.7%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDGSGXXXXXGPTSSDOI 19
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Db 1 MDGSGEQLGSGGPTSSDOI 19

RESULT 8

US-08-856-531-3
Sequence 3, Application US/08856531
Patent No. 5942490
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,531
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, Donald R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..192
OTHER INFORMATION: /note= "Murine BAX polypeptide"
US-08-856-531-3

Query Match 88.5%; Score 69; DB 2; Length 192;
Best Local Similarity 73.7%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDGSGXXXXXGPTSSDOI 19
||||| |||||||
Db 1 MDGSGEQLGSGGPTSSDOI 19

RESULT 9
US-08-856-531-8
Sequence 8, Application US/08856531
Patent No. 5942490
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS

NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,531
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, Donald R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..192
OTHER INFORMATION: /note= "Murine BAX polypeptide"
US-08-856-531-8

Query Match 88.5%; Score 69; DB 2; Length 192;
Best Local Similarity 73.7%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDGSGXXXXXGPTSSDOI 19
||||| |||||||
Db 1 MDGSGEQLGSGGPTSSDOI 19

RESULT 10
US-08-856-034-3
Sequence 3, Application US/08856034
Patent No. 5955595
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,034
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, Donald R.
REGISTRATION NUMBER: 35,197

Db 237 GCGAASSVGGPNGGKQ 252

RESULT 13

US-09-724-676A-82068
; Sequence 82068, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; NUMBER OF SEQ ID NOS: 2000-11-28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82068
; LENGTH: 1054
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-82068

Query Match 46.2%; Score 36; DB 5; Length 1054;
Best Local Similarity 37.5%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 3 GSGXXXXXGPTSSSEQ 18
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Db 237 GCGAASSVGGPNGGKQ 252

RESULT 14

US-09-724-676-82069
; Sequence 82069, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82069
; LENGTH: 1149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-82069

Query Match 46.2%; Score 36; DB 5; Length 1149;
Best Local Similarity 37.5%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 3 GSGXXXXXGPTSSSEQ 18
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Db 237 GCGAASSVGGPNGGKQ 252

RESULT 15

US-09-724-676A-82069
; Sequence 82069, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82069
; LENGTH: 1149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-82069

Query Match 46.2%; Score 36; DB 5; Length 1149;
Best Local Similarity 37.5%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 3 GSGXXXXXGPTSSSEQ 18
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Db 237 GCGAASSVGGPNGGKQ 252

Search completed: January 7, 2003, 12:36:59
Job time : 12.2051 secs

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-423-552-126
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Query Match
Best local Similarity 46.7%; Score 37; DB 7; Length 639;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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Db 623 GGGGSGASGGPTTIE 637
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RESULT 8
US-60-427-579-126
; Sequence 126, Application US/60427579
; GENERAL INFORMATION:
; APPLICANT: American Home Product Inc.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING MAJOR DEPRES
; FILE REFERENCE: AM101250L
; CURRENT APPLICATION NUMBER: US/60/427,579
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 256
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Homo sapiens.
US-60-427-579-126
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Query Match
Best local Similarity 46.7%; Score 37; DB 7; Length 639;
Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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OY 3 GSGXXXXXGGPTSSSE 17
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Db 623 GGGGSGASGGPTTIE 637
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RESULT 9
US-09-134-000C-6041
; Sequence 6041, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6041
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6041
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Query Match
Best local Similarity 47.4%; Score 37; DB 5; Length 748;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 11 GGPTSSSQ 18
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Db 41 GGPTSSSQ 48
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RESULT 10
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US-09-724-676-82011
; Sequence 82011, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82011
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-82011
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Query Match
Best local Similarity 46.2%; Score 36; DB 5; Length 299;
Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
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OY 3 GSGXXXXXGGPTSSSQ 18
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Db 237 GGGAASSVGGPNCCKQ 252
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RESULT 11
US-09-724-676A-82011
; Sequence 82011, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82011
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-82011
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Query Match
Best local Similarity 46.2%; Score 36; DB 5; Length 299;
Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
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OY 3 GSGXXXXXGGPTSSSQ 18
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Db 237 GGGAASSVGGPNCCKQ 252
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RESULT 12
US-09-724-676-82068
; Sequence 82068, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82068
; LENGTH: 1054
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-82068
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```
Query Match
Best local Similarity 46.2%; Score 36; DB 5; Length 1054;
Matches 6; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
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OY 3 GSGXXXXXGGPTSSSQ 18
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:29:58 : Search time 11.2051 Seconds
(without alignments)
120.181 Million cell updates/sec

Title: US-09-876-204-1
Perfect score: 78
Sequence: 1 MDGSGXXXXGPTSSQI 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262191 seqs, 70875818 residues

Total number of hits satisfying chosen parameters: 262191

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	67	85.9	192	1 PCT-US02-38191-5	Sequence 5, Appl
2	67	85.9	192	6 US-10-306-878-5	Sequence 5, Appl
3	62	79.5	191	6 US-10-196-793A-46	Sequence 46, Appl
4	38	48.7	100	6 US-10-264-237-2133	Sequence 2133, Ap
5	37	47.4	639	5 US-09-724-676-64483	Sequence 64483, A
6	37	47.4	639	5 US-09-724-676A-64483	Sequence 64483, A
7	37	47.4	639	7 US-60-423-552-126	Sequence 126, App
8	37	47.4	639	7 US-60-427-579-126	Sequence 126, App
9	37	47.4	748	5 US-09-134-000C-6041	Sequence 6041, App
10	36	46.2	299	5 US-09-724-676-82011	Sequence 82011, A
11	36	46.2	299	5 US-09-724-676A-82011	Sequence 82011, A
12	36	46.2	1054	5 US-09-724-676-82068	Sequence 82068, A
13	36	46.2	1054	5 US-09-724-676A-82068	Sequence 82068, A
14	36	46.2	1149	5 US-09-724-676-82069	Sequence 82069, A
15	36	46.2	1149	5 US-09-724-676A-82069	Sequence 82069, A
16	35	44.9	402	1 PCT-US02-06001-32	Sequence 32, Appl
17	35	44.9	402	6 US-10-274-177-18	Sequence 18, Appl
18	35	44.9	402	6 US-10-087-080-32	Sequence 32, Appl
19	35	44.9	519	5 US-09-724-676-88032	Sequence 88032, A
20	35	44.9	519	5 US-09-724-676A-88032	Sequence 88032, A
21	35	44.9	519	5 US-09-724-676A-88032	Sequence 88032, A
22	35	44.9	519	5 US-09-724-676A-88033	Sequence 88033, A
23	35	44.9	530	5 US-09-724-676-88164	Sequence 88164, A
24	35	44.9	530	5 US-09-724-676A-88164	Sequence 88164, A
25	35	44.9	530	5 US-09-724-676-88168	Sequence 88168, A
26	35	44.9	530	5 US-09-724-676A-88168	Sequence 88168, A

27	35	44.9	530	5	US-09-724-676A-88167	Sequence 88167, A
28	35	44.9	530	5	US-09-724-676A-88168	Sequence 88168, A
29	35	44.9	901	1	PCT-US02-29560-311	Sequence 311, Appl
30	34	43.6	60	5	US-09-646-691B-11	Sequence 11, Appl
31	34	43.6	290	5	US-09-564-951B-4	Sequence 4, Appl
32	34	43.6	290	6	US-10-128-587A-3	Sequence 3, Appl
33	34	43.6	301	6	US-10-128-587A-5	Sequence 5, Appl
34	34	43.6	363	6	US-10-128-587A-98	Sequence 98, Appl
35	34	43.6	373	5	US-09-724-676-78490	Sequence 78490, A
36	34	43.6	373	5	US-09-724-676A-78490	Sequence 78490, A
37	34	43.6	429	5	US-09-134-000C-3817	Sequence 3817, Ap
38	34	43.6	497	5	US-09-724-676-69752	Sequence 69752, A
39	34	43.6	497	5	US-09-724-676A-69752	Sequence 69752, A
40	34	43.6	500	6	US-10-272-983-30	Sequence 30, Appl
41	34	43.6	529	5	US-09-724-676-69753	Sequence 69753, A
42	34	43.6	529	5	US-09-724-676-69754	Sequence 69754, A
43	34	43.6	529	5	US-09-724-676A-69753	Sequence 69753, A
44	34	43.6	529	5	US-09-724-676A-69754	Sequence 69754, A
45	34	43.6	533	7	US-60-423-552-109	Sequence 109, App

ALIGNMENTS

```
RESULT 1
PCT-US02-38191-5
: Sequence 5, Application PC/TUS0238191
: GENERAL INFORMATION:
: APPLICANT: The Burnham Institute
: APPLICANT: Reed, John C.
: TITLE OF INVENTION: Methods for Identifying Modulators of
: TITLE OF INVENTION: Apoptosis
: FILE REFERENCE: FR-LJ 5483
: CURRENT APPLICATION NUMBER: PCT/US02/38191
: CURRENT FILING DATE: 2002-11-27
: PRIOR APPLICATION NUMBER: US 60/334,149
: PRIOR FILING DATE: 2001-11-28
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 192
: TYPE: PRT
: ORGANISM: Homo sapiens
PCT-US02-38191-5

Query Match      85.9%; Score 67; DB 1; Length 192;
Best Local Similarity 73.7%; Pred. No. 0.00015;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 MDGSGXXXXGPTSSQI 19
Db      1 MDGSGEPPRGGPTSSQI 19

RESULT 2
US-10-306-878-5
: Sequence 5, Application US/10306878
: GENERAL INFORMATION:
: APPLICANT: Reed, John C.
: APPLICANT: Guo, Bin
: TITLE OF INVENTION: Methods for Identifying Modulators of
: TITLE OF INVENTION: Apoptosis
: FILE REFERENCE: P-LJ 5535
: CURRENT APPLICATION NUMBER: US/10/306,878
: CURRENT FILING DATE: 2002-11-27
: PRIOR APPLICATION NUMBER: US 60/334,149
: PRIOR FILING DATE: 2001-11-28
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 192
: TYPE: PRT
```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:28:08 : Search time 13.1538 Seconds
(without alignments)
138.861 Million cell updates/sec

Title: US-09-876-204-1

Perfect score: 78

Sequence: 1 MDGSGXXXXXGGPTSSSEQI 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69	88.5	192	2	D47538
2	67	85.9	143	2	I38921
3	67	85.9	179	2	JC7255
4	67	85.9	192	2	A47538
5	67	85.9	218	2	B47538
6	46	59.0	654	2	S27004
7	40	51.3	487	4	S51886
8	40	51.3	492	2	S51885
9	40	51.3	528	4	S51887
10	39	50.0	105	2	PM0018
11	39	50.0	248	2	F86743
12	38	48.7	334	2	A39605
13	38	48.7	487	2	T47107
14	38	48.7	1398	2	T13741
15	38	48.7	2186	2	T13169
16	37.5	48.1	1018	2	T22318
17	37	47.4	321	1	S27501
18	37	47.4	324	2	I81191
19	37	47.4	328	2	S33369
20	37	47.4	580	2	T39122
21	37	47.4	602	1	S38111
22	37	47.4	618	2	PRECT4
23	37	47.4	618	2	H90937
24	37	47.4	618	2	D85786
25	37	47.4	618	2	AB0711
26	37	47.4	639	2	A35719
27	36	46.2	197	2	H86979
28	36	46.2	221	2	T10751
29	36	46.2	276	2	T47351

30	36	46.2	288	2	D85072	hypothetical prote
31	36	46.2	314	2	E86482	protein F55.5 [lm
32	36	46.2	424	2	T10985	regulator protein
33	36	46.2	533	2	T33912	hypothetical prote
34	36	46.2	574	2	T39829	amino-acid permeas
35	36	46.2	1184	2	G01763	atrophin-1 - human
36	36	46.2	1184	2	S50832	atrophin-1 - human
37	36	46.2	1226	2	E84923	hypothetical prote
38	36	46.2	1344	2	T14316	r19-1 protein - mo
39	35	44.9	133	2	AH2405	hypothetical prote
40	35	44.9	240	2	A70657	hypothetical prote
41	35	44.9	347	2	JC7178	chitinase (EC 3.2.
42	35	44.9	436	2	T36706	hypothetical prote
43	35	44.9	473	2	S70357	forward transcrip
44	35	44.9	474	2	S30168	mercury(II) reduct
45	35	44.9	478	2	H83621	pyridine nucleotid

ALIGNMENTS

```
RESULT 1
D47538
bcl-2-associated protein x - mouse
N:Alternate names: BAX; programmed cell death membrane protein x
C:Species: Mus musculus (house mouse)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C:Accession: D47538
R:Olival, Z.N.; Milliman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerate
A:Reference number: A47538; MUID:93364978; PMID:8358790
A:Accession: D47538
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-192 <OLR>
A:Cross-references: GB:L22472
C:Genetics:
A:Gene: bax
C:Superfamily: bcl transforming protein

Query Match      88.5%  Score 69;  DB 2;  Length 192;
Best Local Similarity 73.7%  Pred. No. 1e-05;
Matches 14;  Conservative 0;  Mismatches 5;  Indels 0;  Gaps 0;

QY      1 MDGSGXXXXXGGPTSSSEQI 19
      |||||  |||||
Db      1 MDGSGEQLSGGPTSSSEQI 19

RESULT 2
I38921
bcl-2-associated protein x, delta splice form - human
N:Alternate names: BAX; programmed cell death membrane protein x delta
C:Species: Homo sapiens (man)
C:Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 17-Nov-2000
C:Accession: I38921
R:Apfe, S.S.; Mattei, M.G.; Olsen, B.R.
Genomics 26, 592-594, 1995
A:Title: Mapping of the human BAX gene to chromosome 19q13.3-q13.4 and isolation of a
A:Reference number: I38921; MUID:95331797; PMID:7607685
A:Accession: I38921
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-143 <RES>
A:Cross-references: EMBL:U19599; NID:g841237; PIDN:AAC50142.1; PID:g841238
C:Genetics:
A:Gene: GDB:BAX
A:Cross-references: GDB:228082; OMIM:600040
A:Map position: 19q13.3-19q13.4
C:Superfamily: bcl transforming protein

Query Match      85.9%  Score 67;  DB 2;  Length 143;
```

Best Local Similarity 73.7%; Pred. No. 1.8e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDSSGXXXXGPTSSSQI 19
||||| |||||||||
Db 1 MDSSGEQPRGGGPTSSSQI 19

RESULT 3
JC7255

Bax-delta protein - human

C:Species: Homo sapiens (man)

C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 17-Nov-2000

C:Accession: JC7255

R:Schmitt, E.; Paquet, C.; Beauchemin, M.; Dever-Bertrand, J.; Bertrand, R.

Biochem. Biophys. Res. Commun. 270, 868-879, 2000

A:Title: Characterization of Bax-delta, a cell death-inducing isoform of Bax.

A:Reference number: JC7255

A:Accession: JC7255

A:Molecule type: mRNA

A:Residues: 1-179 <SCH>

A:Cross-references: GB:AF247393

A:Experimental source: cancer promyelocytic cells

C:Comment: This protein, a member of the Bcl-2 family, has a proapoptotic effect. It fun

C:Superfamily: bcl transforming protein

C:Keywords: transmembrane protein

Query Match 85.9%; Score 67; DB 2; Length 179;
Best Local Similarity 73.7%; Pred. No. 2.3e-05;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDSSGXXXXGPTSSSQI 19
||||| |||||||||
Db 1 MDSSGEQPRGGGPTSSSQI 19

RESULT 4
A47538

bcl-2-associated protein x, alpha splice form - human

N:Alternate names: BAX; programmed cell death membrane protein x alpha

C:Species: Homo sapiens (man)

C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000

C:Accession: A47538

R:Oltvai, Z.N.; Millman, C.L.; Korsmeyer, S.J.

Cell 74, 609-619, 1993

A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates F

A:Reference number: A47538; MUID:93364978; PMID:8358790

A:Accession: A47538

A:Molecule type: mRNA

A:Residues: 1-192 <OLT>

A:Cross-references: GB:L22473; NID:q388165; PIDN:AAA03619.1; PID:q388166

A:Note: the amino end of the mature protein is blocked

C:Genetics:

A:Gene: GDB:BAX

A:Cross-references: GDB:228082; OMIM:600040

A:Map position: 19q13.3-19q13.4

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; blocked amino end; heterodimer; homodimer; transmembr

F;172-191/Domain: transmembrane #status predicted <TM1>

Query Match 85.9%; Score 67; DB 2; Length 192;
Best Local Similarity 73.7%; Pred. No. 2.5e-05;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDSSGXXXXGPTSSSQI 19
||||| |||||||||
Db 1 MDSSGEQPRGGGPTSSSQI 19

RESULT 5
B47538

bcl-2-associated protein x, beta splice form - human

N:Alternate names: BAX; programmed cell death membrane protein x beta

C:Species: Homo sapiens (man)

C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000

C:Accession: B47538

R:Oltvai, Z.N.; Millman, C.L.; Korsmeyer, S.J.

Cell 74, 609-619, 1993

A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerate

A:Reference number: A47538; MUID:93364978; PMID:8358790

A:Accession: B47538

A:Molecule type: mRNA

A:Residues: 1-218 <OLT>

A:Cross-references: GB:L22474; NID:q388167; PIDN:AAA03620.1; PID:q388168

A:Note: the amino end of the mature protein is blocked

C:Genetics:

A:Gene: GDB:BAX

A:Cross-references: GDB:228082; OMIM:600040

A:Map position: 19q13.3-19q13.4

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; blocked amino end; cytosol; heterodimer; homodimer

Query Match 85.9%; Score 67; DB 2; Length 218;
Best Local Similarity 73.7%; Pred. No. 2.9e-05;

Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDSSGXXXXGPTSSSQI 19
||||| |||||||||
Db 1 MDSSGEQPRGGGPTSSSQI 19

RESULT 6
S27004

dnak-lype molecular chaperone hsp70.1 - Hydra magnipapillata

N:Alternate names: heat shock protein 70.1

C:Species: Hydra magnipapillata

A:Variety: strain 105

C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Aug-1999

C:Accession: S27004

R:Gelliner, K.; Praetzel, G.; Bosch, T.C.G.

Eur. J. Biochem. 210, 683-691, 1992

A:Title: Cloning and expression of a heat-inducible hsp70 gene in two species of Hydr

A:Reference number: S27004; MUID:93130891; PMID:1483453

A:Accession: S27004

A:Molecule type: DNA

A:Residues: 1-654

A:Cross-references: EMBL:M84019; NID:g159267; PIDN:AAA29213.1; PID:g159268

C:Genetics:

A:Gene: hsp70.1

A:Insertions: 69/1; 93/3

C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein co

C:Superfamily: heat shock protein 70

C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 59.0%; Score 46; DB 2; Length 654;
Best Local Similarity 52.9%; Pred. No. 1.1;

Matches 9; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 MDSSGXXXXGPTSSSE 17
||| |||||
Db 636 MPSSGKASSGPTIEE 652

RESULT 7
S51886

hypothetical protein HRX1851.1 - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 05-May-1995 #sequence_revision 05-Sep-1996 #text_change 20-Oct-2000

C:Accession: S59162; S51886

R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.

Yeast 11, 1069-1075, 1995

A:Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including t

a delta element.

A:Reference number: S59162; MUID:96076631; PMID:7502582

A:Accession: S59162
A:Status: nucleic acid sequence not shown; translation not shown; conceptual translation
A:Molecule type: DNA
A:Residues: 1-487 <VAM>
A:Cross-references: EMBL:248149; NID:9663234; PIDN:CAA8149.1; PID:9663241
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
C:Comment: There is no evidence that this sequence is expressed.
C:Genetics:
A:Map position: 15L
A:Introns: 472/2
C:Keywords: pseudogene

Query Match 51.3%; Score 40; DB 4; Length 487;
Best Local Similarity 38.9%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 MDGSGXXXXGGPTSSQ 18
1:1:1 1111:
Db 310 MNGNGSTDQISGPASGEE 327

RESULT 8
S51885
Probable membrane protein YOL112w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein HRC492; hypothetical protein O0726
C:Species: Saccharomyces cerevisiae
C:Date: 05-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jul-2000
C:Accession: S51885; S59161; S66808
R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Submitted to the EMBL Data Library, January 1995
A:Description: Sequence analysis of a 44kb DNA fragment of yeast chromosome XV including and a Delta.
A:Reference number: S51848
A:Accession: S51885
A:Molecule type: DNA
A:Residues: 1-492 <VAM>
A:Cross-references: EMBL:248149; NID:9663234; PID:9663240
R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Yeast 11, 1069-1075, 1995
A:Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including the a delta element.
A:Reference number: S59156; MUID:96076631; PMID:7502582
A:Accession: S59161
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-492 <VAM>
A:Cross-references: EMBL:248149; NID:9663234; PIDN:CAA8148.1; PID:9663240
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
R:Durand, P.; Hilger, F.; Portetelle, D.; Vandenbol, M.
Submitted to the Protein Sequence Database, July 1996
A:Reference number: S66791
A:Accession: S66808
A:Molecule type: DNA
A:Residues: 1-492 <DOR>
A:Cross-references: EMBL:274854; NID:91419980; PID:91419981; MIPS:YOL112w
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:MSB4
A:Cross-references: SGD:S0005472; MIPS:YOL112w
A:Map position: 15L
C:Superfamily: Saccharomyces probable membrane protein YOL112w
C:Keywords: transmembrane protein
F:238-254/Domain: transmembrane #status predicted <TM1>
F:335-351/Domain: transmembrane #status predicted <TM2>

Query Match 51.3%; Score 40; DB 2; Length 492;
Best Local Similarity 38.9%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 MDGSGXXXXGGPTSSQ 18
1:1:1 1111:
Db 310 MNGNGSTDQISGPASGEE 327

RESULT 9
S51887
Hypothetical protein HRX1851.2 - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 05-May-1995 #sequence_revision 05-Sep-1996 #text_change 20-Oct-2000
C:Accession: S59163; S51887
R:Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Yeast 11, 1069-1075, 1995
A:Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including a delta element.
A:Reference number: S59156; MUID:96076631; PMID:7502582
A:Accession: S59163
A:Status: nucleic acid sequence not shown; translation not shown; conceptual translation
A:Molecule type: DNA
A:Residues: 1-528 <VAM>
A:Cross-references: EMBL:248149; NID:9663234; PIDN:CAA8150.1; PID:9663242
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
C:Comment: There is no evidence that this sequence is expressed.
C:Genetics:
A:Map position: 15L
A:Introns: 472/2
C:Keywords: pseudogene

Query Match 51.3%; Score 40; DB 4; Length 528;
Best Local Similarity 38.9%; Pred. No. 12;
Matches 7; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 MDGSGXXXXGGPTSSQ 18
1:1:1 1111:
Db 310 MNGNGSTDQISGPASGEE 327

RESULT 10
PM0018
Hypothetical protein 105 - Micromonospora sp. (fragment)
C:Species: Micromonospora sp.
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Oct-1994
C:Accession: PM0018
R:Kleimen, G.H.; Cundliffe, E.; Financsek, I.
Gene 98, 53-60, 1991
A:Title: Cloning and characterization of gentamicin-resistance genes from Micromonospora
A:Reference number: JG0017; MUID:91192615; PMID:2013410
A:Accession: PM0018
A:Molecule type: DNA
A:Residues: 1-105 <REL>
A:Cross-references: GB:M55521
A:Note: the authors translated the codon CCG for residues 27, 30, 31, and 37 as Phe a

Query Match 50.0%; Score 39; DB 2; Length 105;
Best Local Similarity 61.5%; Pred. No. 3;2;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 4 SCGXXXXGGPTSS 16
11 111111
Db 74 SCGVAATGGPTSS 86

RESULT 11
F86743
Hypothetical protein daCB [imported] - Lactococcus lactis subsp. lactis (strain IL140
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: F86743
R:Boilotin, A.; Wincker, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Eh
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A:Reference number: AB6625; MUID:21235186; PMID:11337471
A:Accession: F86743
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <STO>
A:Cross-references: GB:AF005176; PID:912723887; PIDN:AAK05048.1; GSPDB:GN00146

A:Experimental source: strain IL1403
C:Genetics:
A:Gene: dacB

Query Match 50.0%; Score 39; DB 2; Length 248;
Best Local Similarity 38.9%; Pred. No. 8.2;
Matches 7; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Oy 1 MDGSGXXXXXGCPRSSQ 18
Db 134 MNGGTYNSSGNPISFEE 151

RESULT 12

A39605 transcription regulator php2, HAP2 homolog - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe
C>Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 31-Jan-2000

C:Accession: A39605; T40663

R:Olesen, J.T.; Fikes, J.D.; Guarente, L.
Mol. Cell. Biol. 11, 611-619, 1991

A:Title: The Schizosaccharomyces pombe homolog of Saccharomyces cerevisiae HAP2 reveals
A:Reference number: A39605; MUID:91117227; PMID:1899284

A:Accession: A39605

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-334 <OLE>

A:Cross-references: GB:M63639; NID:9173424; PIDN:AAA3322.1; PID:9173425
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, November 1998

A:Reference number: Z21889

A:Accession: T40663

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-334 <LYN>

A:Cross-references: EMBL:AL034352; PIDN:CAA22183.1; GSPDB:GN00067; SPDB:SPBC725.11c
A:Experimental source: strain 972h-; cosmid c725

C:Genetics:

A:Gene: SPBC725.11c

A:Map position: 2
C:Keywords: DNA binding; nucleus; transcription regulation

Query Match 48.7%; Score 38; DB 2; Length 334;
Best Local Similarity 43.8%; Pred. No. 18;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Oy 1 MDGSGXXXXXGCPRSS 16
Db 165 LDMSGNIMSGCPYNT 180

RESULT 13

T47107 benzaldehyde dehydrogenase (NAD) (EC 1.2.1.28) [validated] - Pseudomonas putida plasmid

C:Species: Pseudomonas putida
C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 03-Jun-2002

C:Accession: T47107; S13388

R:Inoue, J.; Shaw, J.P.; Reikik, M.; Harayama, S.
J. Bacteriol. 177, 1196-1201, 1995

A:Title: Overlapping substrate specificity of benzaldehyde dehydrogenase (the xylC gene
Pseudomonas putida.
A:Reference number: Z24352; MUID:95173094; PMID:7868591

A:Accession: T47107

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1487 <INO>

A:Cross-references: EMBL:U15151; NID:9555994; PIDN:AAA66218.1; PID:9555995
R:Chalmers, R.M.; Keen, J.N.; Fewson, C.A.
Biochem. J. 273, 99-107, 1991

A:Title: Comparison of benzyl alcohol dehydrogenases and benzaldehyde dehydrogenases from
uene pathway in Pseudomonas putida.
A:Reference number: S13298; MUID:91113163; PMID:1899592

A:Accession: S13388

A:Molecule type: protein
A:Residues: 1-44 <CHA>
A:Experimental source: strain MT53

C:Genetics:

A:Gene: xylC

A:Genome: plasmid

A>Note: TOL plasmid pWMO

C:Function:
A:Description: EC 1.2.1.28 [validated, MUID:95173094]

A:Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology
C:Keywords: oxidoreductase

Query Match 48.7%; Score 38; DB 2; Length 487;
Best Local Similarity 44.4%; Pred. No. 27;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Oy 1 MDGSGXXXXXGCPRSSQ 18
Db 452 MGASGSGRFGPASTIE 469

RESULT 14

T13741 hypothetical protein 22E5.8 - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C:Accession: T13741

R:Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999

A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: Z17668

A:Accession: T13741

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1398 <MUR>

A:Cross-references: EMBL:AL031765; NID:e1371523; PID:e1329905; PIDN:CAA21125.1
A:Introns: 205/3; 227/1; 322/3; 688/3; 782/3; 814/2; 1363/3

A:Note: EG:22E5.8

Query Match 48.7%; Score 38; DB 2; Length 1398;
Best Local Similarity 50.0%; Pred. No. 87;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Oy 2 DGSGXXXXXGCPPTS 15
Db 851 MGSGSGNANGCPPTS 864

RESULT 15

T13169 tigrin - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C:Accession: T13169

R:Fogarty, F.J.; Fessler, L.I.; Bunch, T.A.; Yaron, Y.; Parker, C.G.; Nelson, R.E.; B
Development 120, 1747-1758, 1994

A:Title: Tigrin, a novel Drosophila extracellular matrix protein that functions as a
A:Reference number: Z17625; MUID:95009506; PMID:7924982

A:Accession: T13169

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2186 <FOG>

A:Cross-references: EMBL:U09506; NID:9493069; PID:9493070; PIDN:AAA56998.1
A:Cross-references: FlyBase:FBgn0011722

C:Function:
A:Description: functions as a ligand for Drosophila alpha P52 beta PS integrins

Query Match 48.7%; Score 38; DB 2; Length 2186;
Best Local Similarity 50.0%; Pred. No. 14e+02;
Matches 7; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 GSGXXXXGGPTSS 16
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Db 2057 GSAASASGGPTGS 2070

Search completed: January 7, 2003, 12:31:20
Job time : 15.1538 secs

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RESULT 2
PCT-US99-24747-2
; Sequence 2, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US99-24747-2

Query Match      88.5%; Score 69; DB 1; Length 70;
Best Local Similarity 73.7%; Pred. No. 0.00031;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDGSGXXXXXGGPTSSSEQI 19
Db 1 MDGSGEQLGSGGPTSSSEQI 19

RESULT 3
PCT-US99-24747-6
; Sequence 6, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US99-24747-6

Query Match      88.5%; Score 69; DB 1; Length 70;
Best Local Similarity 73.7%; Pred. No. 0.00031;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDGSGXXXXXGGPTSSSEQI 19
Db 1 MDGSGEQLGSGGPTSSSEQI 19

RESULT 4
US-09-177-315-2
; Sequence 2, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-5756
; CURRENT APPLICATION NUMBER: US/09/177,315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-177-315-2

Query Match      88.5%; Score 69; DB 15; Length 70;
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Best Local Similarity 73.7%; Pred. No. 0.00031;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDGSGXXXXXGGPTSSSEQI 19
Db 1 MDGSGEQLGSGGPTSSSEQI 19

RESULT 5
US-09-177-315-6
; Sequence 6, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-5756
; CURRENT APPLICATION NUMBER: US/09/177,315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 6
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-177-315-6

Query Match      88.5%; Score 69; DB 15; Length 70;
Best Local Similarity 73.7%; Pred. No. 0.00031;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDGSGXXXXXGGPTSSSEQI 19
Db 1 MDGSGEQLGSGGPTSSSEQI 19

RESULT 6
PCT-US99-24747-4
; Sequence 4, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 4
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US99-24747-4

Query Match      88.5%; Score 69; DB 1; Length 78;
Best Local Similarity 73.7%; Pred. No. 0.00031;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDGSGXXXXXGGPTSSSEQI 19
Db 1 MDGSGEQLGSGGPTSSSEQI 19

RESULT 7
PCT-US99-24747-8
; Sequence 8, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
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SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US99-24747-8

Query Match 88.5%; Score 69; DB 1; Length 78;
Best Local Similarity 73.7%; Pred. No. 0.00035;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDGSGXXXXGGPTSSEQI 19
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DB 1 MDGSGEQLGSGGPTSSEQI 19

RESULT 8
US-09-177-315-4
; Sequence 4, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachel M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-5756
; CURRENT APPLICATION NUMBER: US/09/177,315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-177-315-4

Query Match 88.5%; Score 69; DB 15; Length 78;
Best Local Similarity 73.7%; Pred. No. 0.00035;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDGSGXXXXGGPTSSEQI 19
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DB 1 MDGSGEQLGSGGPTSSEQI 19

RESULT 9
US-09-177-315-8
; Sequence 8, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachel M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-5756
; CURRENT APPLICATION NUMBER: US/09/177,315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-177-315-8

Query Match 88.5%; Score 69; DB 15; Length 78;
Best Local Similarity 73.7%; Pred. No. 0.00035;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDGSGXXXXGGPTSSEQI 19
||||| |||||||||
DB 1 MDGSGEQLGSGGPTSSEQI 19

RESULT 10
PCT-US98-19765-45
; Sequence 45, Application PC/TUS9819765

GENERAL INFORMATION:
; APPLICANT: WASHINGTON UNIVERSITY
; TITLE OF INVENTION: CELL DEATH AGONISTS
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/19765
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: HENDERSON, MELODIE W
; REGISTRATION NUMBER: 37,848
; REFERENCE/DOCKET NUMBER: 6029-6526
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US98-19765-45

Query Match 88.5%; Score 69; DB 1; Length 192;
Best Local Similarity 73.7%; Pred. No. 0.00096;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDGSGXXXXGGPTSSEQI 19
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DB 1 MDGSGEQLGSGGPTSSEQI 19

RESULT 11
PCT-US99-24747-13
; Sequence 13, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachel M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US99-24747-13

Query Match 88.5%; Score 69; DB 1; Length 192;
Best Local Similarity 73.7%; Pred. No. 0.00096;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDGSGXXXXGGPTSSEQI 19
||||| |||||||||
DB 1 MDGSGEQLGSGGPTSSEQI 19

RESULT 12

US-08-112-208B-5
; Sequence 5, Application US/08112208B
; GENERAL INFORMATION:
; APPLICANT: Korsmeyer, Stanley J.
; TITLE OF INVENTION: Cell Death Regulators
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/112,208B
; FILING DATE: 26-AUG-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; US-08-112-208B-5

Query Match 88.5%; Score 69; DB 5; Length 192;
Best Local Similarity 73.7%; Pred. No. 0.00096;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDGSGXXXXGGPTSSDOI 19
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Db 1 MDGSGEQLGSGGPTSSDOI 19

RESULT 13
US-08-248-819-5
; Sequence 5, Application US/08248819
; GENERAL INFORMATION:
; APPLICANT: Korsmeyer, Stanley J.
; TITLE OF INVENTION: Cell Death Regulators
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,819
; FILING DATE: 25-MAY-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; NAME/KEY: Protein
; LOCATION: 1..192
; OTHER INFORMATION: /note= "Protein sequence of murine

NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-6-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
US-08-248-819-5

Query Match 88.5%; Score 69; DB 6; Length 192;
Best Local Similarity 73.7%; Pred. No. 0.00096;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDGSGXXXXGGPTSSDOI 19
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Db 1 MDGSGEQLGSGGPTSSDOI 19

RESULT 14
US-08-483-233-3
; Sequence 3, Application US/08483233
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,233
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,646
; FILING DATE: 10-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,819
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000640
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; NAME/KEY: Protein
; LOCATION: 1..192
; OTHER INFORMATION: /note= "Protein sequence of murine

OTHER INFORMATION: Bax.."
US-08-483-233-3

Query Match 88.5%; Score 69; DB 8; Length 192;
Best Local Similarity 73.7%; Pred. No. 0.00096;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDGSGXXXXXGGPTSSSEQI 19
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Db 1 MDGSGEQLGSGGPTSSSEQI 19
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RESULT 15

US-08-483-233-8
; Sequence 8, Application US/08483233
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,233
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,646
; FILING DATE: 10-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,819
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000640
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-233-8

Query Match 88.5%; Score 69; DB 8; Length 192;
Best Local Similarity 73.7%; Pred. No. 0.00096;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 1 MDGSGEQLGSGGPTSSSEQI 19

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Job time : 134 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:30:53 : Search time 7.30769 Seconds
(without alignments)
49.274 Million cell updates/sec

Title: US-09-876-204-1

Perfect score: 78
Sequence: 1 MDGSGXXXXGGPTSSFOI 19

Scoring table:

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Gapop 10.0, Capext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	68	87.2	19	US-09-876-204-1	Sequence 1, Appli
3	68	87.2	20	US-09-876-204-5	Sequence 5, Appli
4	67	85.9	20	US-09-876-204-3	Sequence 3, Appli
5	64	82.1	331	US-09-031-525-2	Sequence 2, Appli
6	38	48.7	154	US-09-876-889-16	Sequence 16, Appli
7	36	46.2	500	US-09-766-378A-25	Sequence 25, Appli
8	36	46.2	547	US-09-815-837-90	Sequence 90, Appli
9	36	46.2	553	US-09-815-837-50	Sequence 50, Appli
10	36	46.2	555	US-09-815-837-71	Sequence 71, Appli
11	36	46.2	559	US-09-815-837-96	Sequence 96, Appli
12	36	46.2	560	US-09-815-837-73	Sequence 73, Appli
13	36	46.2	562	US-09-815-837-70	Sequence 70, Appli
14	36	46.2	676	US-09-815-837-69	Sequence 69, Appli
15	36	46.2	678	US-09-815-837-68	Sequence 68, Appli
16	36	46.2	772	US-09-815-837-74	Sequence 74, Appli
17	36	46.2	774	US-09-815-837-72	Sequence 72, Appli
18	35	44.9	46	US-09-989-919-115	Sequence 115, Appli
19	35	44.9	473	US-09-844-353A-99	Sequence 99, Appli

20	35	44.9	593	9	US-09-964-899-15	Sequence 15, Appli
21	35	44.9	646	9	US-09-964-899-17	Sequence 17, Appli
22	35	44.9	645	9	US-09-964-899-53	Sequence 53, Appli
23	35	44.9	850	10	US-09-985-675-2	Sequence 2, Appli
24	35	44.9	874	10	US-09-985-675-1	Sequence 1, Appli
25	35	44.9	880	10	US-09-223-490-10	Sequence 10, Appli
26	34.5	44.2	258	9	US-09-738-626-4896	Sequence 4896, Ap
27	34	43.6	121	9	US-10-061-395-75	Sequence 75, Appli
28	34	43.6	127	10	US-09-916-940-43	Sequence 43, Appli
29	34	43.6	171	9	US-10-061-395-76	Sequence 76, Appli
30	34	43.6	177	10	US-09-916-940-44	Sequence 44, Appli
31	34	43.6	314	9	US-09-973-025-42	Sequence 42, Appli
32	34	43.6	319	9	US-09-973-025-44	Sequence 44, Appli
33	34	43.6	338	9	US-09-973-025-38	Sequence 38, Appli
34	34	43.6	343	9	US-09-973-025-40	Sequence 40, Appli
35	34	43.6	344	10	US-09-925-301-967	Sequence 967, App
36	34	43.6	398	10	US-09-815-333-2	Sequence 2, Appli
37	34	43.6	398	10	US-09-842-316-2	Sequence 2, Appli
38	34	43.6	398	12	US-10-037-616-26	Sequence 26, Appli
39	34	43.6	437	12	US-10-016-358-2	Sequence 2, Appli
40	34	43.6	463	9	US-09-973-025-46	Sequence 46, Appli
41	34	43.6	490	9	US-09-973-025-36	Sequence 36, Appli
42	34	43.6	506	10	US-09-976-165-19	Sequence 19, Appli
43	34	43.6	692	9	US-09-973-025-48	Sequence 48, Appli
44	34	43.6	790	10	US-09-801-368-184	Sequence 184, App
45	34	43.6	809	9	US-09-973-025-50	Sequence 50, Appli

ALIGNMENTS

RESULT 1
US-09-876-204-4
: Sequence 4, Application US/09876204
: Patent No. US20020052316A1
: GENERAL INFORMATION:
: APPLICANT: Gordon C. Shore et al.
: TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
: FILE REFERENCE: 50013/011001
: CURRENT APPLICATION NUMBER: US/09/876, 204
: CURRENT FILING DATE: 2001-06-06
: PRIOR APPLICATION NUMBER: 09/166, 028
: PRIOR FILING DATE: 1998-10-05
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-876-204-4

Query Match 88.5%; Score 69; DB 10; Length 20;
Best Local Similarity 73.7%; Pred. No. 9.2e-06;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0:

QY 1 MDGSGXXXXGGPTSSFOI 19
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DB 1 MDGSGDGLGSGPTSSFOI 19

RESULT 2
US-09-876-204-1
: Sequence 1, Application US/09876204
: Patent No. US20020052316A1
: GENERAL INFORMATION:
: APPLICANT: Gordon C. Shore et al.
: TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
: FILE REFERENCE: 50013/011001
: CURRENT APPLICATION NUMBER: US/09/876, 204
: CURRENT FILING DATE: 2001-06-06
: PRIOR APPLICATION NUMBER: 09/166, 028


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Db 72 LEGSGSAGEGKPALEE 89
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RESULT 7
US-09-766-378A-25
; Sequence 25, Application US/09766378A
; Patent No. US20020091079A1
; GENERAL INFORMATION:
; APPLICANT: Rhode, Peter R.
; Acevedo, Jorge
; Burkhardt, Martin
; Jiao, Jin-an
; Mong, Hing C.
; TITLE OF INVENTION: SOLUBLE MHC COMPLEXES AND
; METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: usa
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/766,378A
; FILING DATE: 19-Jan-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/960,190
; FILING DATE: 29-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Corless, Peter F.
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 48002-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 500 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-766-378A-25

Query Match 46.2%; Score 36; DB 10; Length 500;
Best Local Similarity 53.3%; Pred. No. 73;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 GSGGXXXXGPTSSSE 17
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Db 254 GSGGGGSGGGSSSE 268

RESULT 8
US-09-815-837-90
; Sequence 90, Application US/09815837
; Patent No. US20020082411A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Darrick
; APPLICANT: Zhu, Shirley
; APPLICANT: Arimilli, Subhashini
; APPLICANT: Wang, Aijun
```

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; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Immune Mediators and Related Methods
; FILE REFERENCE: 014058-005670US
; CURRENT APPLICATION NUMBER: US/09/815,837
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,274
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/204,249
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/264,003
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:PCRC188
; OTHER INFORMATION: recombinant MHC class II heterodimer
US-09-815-837-90

Query Match 46.2%; Score 36; DB 10; Length 547;
Best Local Similarity 53.3%; Pred. No. 79;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 GSGGXXXXGPTSSSE 17
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Db 235 GSGGGGSGGGSSSE 249

RESULT 9
US-09-815-837-50
; Sequence 50, Application US/09815837
; Patent No. US20020082411A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Darrick
; APPLICANT: Zhu, Shirley
; APPLICANT: Arimilli, Subhashini
; APPLICANT: Wang, Aijun
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Immune Mediators and Related Methods
; FILE REFERENCE: 014058-005670US
; CURRENT APPLICATION NUMBER: US/09/815,837
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,274
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/204,249
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/264,003
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:I- As
; OTHER INFORMATION: MBP.betalactamphalaphaz.Ck single chain
; OTHER INFORMATION: molecule
US-09-815-837-50

Query Match 46.2%; Score 36; DB 10; Length 553;
Best Local Similarity 53.3%; Pred. No. 80;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 GSGGXXXXGPTSSSE 17
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Db 241 GSGGGGSGGGSSSE 255

RESULT 10
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US-09-815-837-71
; Sequence 71, Application US/09815837
; Patent No. US20020082411A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Derrick
; APPLICANT: Zhu, Shirley
; APPLICANT: Arimilli, Subhashini
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: Immune Medators and Related Methods
; FILE REFERENCE: 014058-005670US
; CURRENT APPLICATION NUMBER: US/09/815,837
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,274
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/204,249
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/264,003
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: IAS MBP 90-101
; OTHER INFORMATION: CH1.H recombinant MHC class II-peptide-Ig fusion
US-09-815-837-71

Query Match 46.2%; Score 36; DB 10; Length 555;
Best Local Similarity 53.3%; Pred. No. 80;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 3 GSGGXXXXGGTSSSE 17
Db 243 GSGGGGSGGGSSSE 257

RESULT 11
US-09-815-837-96
; Sequence 96, Application US/09815837
; Patent No. US20020082411A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Derrick
; APPLICANT: Zhu, Shirley
; APPLICANT: Arimilli, Subhashini
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: Immune Medators and Related Methods
; FILE REFERENCE: 014058-005670US
; CURRENT APPLICATION NUMBER: US/09/815,837
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,274
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/204,249
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/264,003
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCB220
; OTHER INFORMATION: recombinant MHC class II heterodimer
US-09-815-837-96

Query Match 46.2%; Score 36; DB 10; Length 559;
Best Local Similarity 53.3%; Pred. No. 81;

Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
OY 3 GSGGXXXXGGTSSSE 17
Db 247 GSGGGGSGGGSSSE 261

RESULT 12
US-09-815-837-73
; Sequence 73, Application US/09815837
; Patent No. US20020082411A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Derrick
; APPLICANT: Zhu, Shirley
; APPLICANT: Arimilli, Subhashini
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: Immune Medators and Related Methods
; FILE REFERENCE: 014058-005670US
; CURRENT APPLICATION NUMBER: US/09/815,837
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,274
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/204,249
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/264,003
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: IAS MBP 1-14
; OTHER INFORMATION: CH1.H.CH2 recombinant MHC class II-peptide-Ig
US-09-815-837-73

Query Match 46.2%; Score 36; DB 10; Length 560;
Best Local Similarity 53.3%; Pred. No. 81;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 3 GSGGXXXXGGTSSSE 17
Db 243 GSGGGGSGGGSSSE 257

RESULT 13
US-09-815-837-70
; Sequence 70, Application US/09815837
; Patent No. US20020082411A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Derrick
; APPLICANT: Zhu, Shirley
; APPLICANT: Arimilli, Subhashini
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: Immune Medators and Related Methods
; FILE REFERENCE: 014058-005670US
; CURRENT APPLICATION NUMBER: US/09/815,837
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,274
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/204,249
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/264,003
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 562
; TYPE: PRT

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:38:59 : Search time 11.7949 Seconds
(without alignments)
120.181 Million cell updates/sec

Title: US-09-876-204-3

Perfect score: 20
Sequence: 1 MDGSGEOPRGCGPTSSEQIM 20

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 262191 seqs, 70875818 residues

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database :

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6: /cgn2_6/plodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/plodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	192	1	PCT-US02-38191-5
2	20	100.0	192	6	US-10-306-878-5
3	19	95.0	191	6	US-10-196-793A-46
4	6	30.0	68	5	US-09-134-000C-4348
5	6	30.0	94	1	PCT-US02-32727-10714
6	6	30.0	94	6	US-10-057-498-10714
7	6	30.0	120	6	US-10-092-411A-5332
8	6	30.0	134	7	US-60-425-158-26
9	6	30.0	155	7	US-60-425-158-23
10	6	30.0	155	7	US-60-425-158-31
11	6	30.0	174	7	US-60-425-158-38
12	6	30.0	176	7	US-60-425-158-28
13	6	30.0	195	7	US-60-425-158-35
14	6	30.0	195	7	US-60-425-158-49
15	6	30.0	220	5	US-09-724-676A-55403
16	6	30.0	220	5	US-09-724-676A-55403
17	6	30.0	413	5	US-09-724-676A-97063
18	6	30.0	413	5	US-09-724-676A-97063
19	6	30.0	413	5	US-09-724-676A-97063
20	6	30.0	586	5	US-10-258-951-54
21	6	30.0	748	5	US-09-134-000C-6041
22	6	30.0	4219	6	US-10-085-198-2
23	5	25.0	16	6	US-10-308-128-65
24	5	25.0	21	7	US-60-427-045-298
25	5	25.0	45	6	US-10-276-774-2564
26	5	25.0	49	6	US-10-203-138A-13021

27	5	25.0	49	6	US-10-218-102-365	Sequence 365, App
28	5	25.0	50	1	PCT-US02-32727-19622	Sequence 19622, A
29	5	25.0	50	6	US-10-057-498-19622	Sequence 19622, A
30	5	25.0	52	1	PCT-US02-32727-18710	Sequence 18710, A
31	5	25.0	52	6	US-10-057-498-18710	Sequence 18710, A
32	5	25.0	53	6	US-10-276-781-1619	Sequence 1619, Ap
33	5	25.0	54	1	PCT-US02-32727-6231	Sequence 6231, Ap
34	5	25.0	54	5	US-09-724-676A-52306	Sequence 52306, A
35	5	25.0	54	5	US-09-724-676A-52306	Sequence 52306, A
36	5	25.0	54	6	US-10-057-498-6231	Sequence 6231, Ap
37	5	25.0	55	1	PCT-US02-32727-25053	Sequence 25053, A
38	5	25.0	55	6	US-10-057-498-25053	Sequence 25053, A
39	5	25.0	56	1	PCT-US02-32727-22223	Sequence 22223, A
40	5	25.0	56	6	US-10-057-498-22223	Sequence 22223, A
41	5	25.0	57	1	PCT-US02-32727-3527	Sequence 3527, Ap
42	5	25.0	57	6	US-10-057-498-3527	Sequence 3527, Ap
43	5	25.0	58	1	PCT-US02-32727-16184	Sequence 16184, A
44	5	25.0	58	1	PCT-US02-32727-17216	Sequence 17216, A
45	5	25.0	58	6	US-10-057-498-16184	Sequence 16184, A

ALIGNMENTS

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RESULT 1
PCT-US02-38191-5
: Sequence 5, Application PC/TUS0238191
: GENERAL INFORMATION:
: APPLICANT: The Burnham Institute
: APPLICANT: Reed, John C.
: APPLICANT: Guo, Bin
: TITLE OF INVENTION: Methods for Identifying Modulators of
: Apoptosis
: FILE REFERENCE: EP-LJ 5483
: CURRENT APPLICATION NUMBER: PCT/US02/38191
: PRIOR FILING DATE: 2002-11-27
: PRIOR APPLICATION NUMBER: US 60/334,149
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 192
: TYPE: PRT
: ORGANISM: Homo sapiens
PCT-US02-38191-5

Query Match          100.0%  Score 20:  DB 1:  Length 192:
Best Local Similarity 100.0%:  Pred. No. 7.4e-12:
Matches 20:  Conservative 0:  Mismatches 0:  Indels 0:  Gaps 0:

QY 1 MDGSGEOPRGCGPTSSEQIM 20
Db 1 MDGSGEOPRGCGPTSSEQIM 20

RESULT 2
US-10-306-878-5
: Sequence 5, Application US/10306878
: GENERAL INFORMATION:
: APPLICANT: Reed, John C.
: APPLICANT: Guo, Bin
: TITLE OF INVENTION: Methods for Identifying Modulators of
: Apoptosis
: FILE REFERENCE: P-LJ 5335
: CURRENT APPLICATION NUMBER: US/10/306,878
: PRIOR FILING DATE: 2002-11-27
: PRIOR APPLICATION NUMBER: US 60/334,149
: PRIOR FILING DATE: 2001-11-28
: NUMBER OF SEQ ID NOS: 28
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 192
: TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-306-878-5

Query Match 100.0%; Score 20; DB 6; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.4e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGCGPTSSSEQIM 20
Db 1 MDGSGEOPRGCGPTSSSEQIM 20

RESULT 3
US-10-196-793A-46
; Sequence 46, Application US/10196793A
; GENERAL INFORMATION:
; APPLICANT: ROSENBLUM, MARTIN G.
; APPLICANT: LIU, YUYING
; TITLE OF INVENTION: THERAPEUTIC AGENTS COMPRISING PRO-APOPTOTIC PROTEINS
; FILE REFERENCE: CLFR:012US
; CURRENT APPLICATION NUMBER: US/10/196,793A
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 60/360,361
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/332,886
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/306,091
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-196-793A-46

Query Match 95.0%; Score 19; DB 6; Length 191;
Best Local Similarity 100.0%; Pred. No. 6.4e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGSGEOPRGCGPTSSSEQIM 20
Db 1 DGSGEOPRGCGPTSSSEQIM 19

RESULT 4
US-09-134-000C-4348
; Sequence 4348, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4348
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (44)..(44)
; OTHER INFORMATION: Amino acid 44 is Xaa wherein Xaa = any amino acid.
US-09-134-000C-4348

Query Match 30.0%; Score 6; DB 5; Length 68;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 GGGPTS 15
Db 25 GGGPTS 30

RESULT 5
PCT-US02-32727-10714
; Sequence 10714, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yann
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514c1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 10714
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Propionibacterium
PCT-US02-32727-10714

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Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 GPTSSE 17
Db 30 GPTSSE 35

RESULT 6
US-10-057-498-10714
; Sequence 10714, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 10714
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Propionibacterium
US-10-057-498-10714

Query Match 30.0%; Score 6; DB 6; Length 94;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 GPTSSE 17
Db 30 GPTSSE 35

RESULT 7
US-10-092-411A-5332
; Sequence 5332, Application US/10092411A

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; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-101
; CURRENT APPLICATION NUMBER: US/10/092,411A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5676
; SEQ ID NO 5332
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-5332

Query Match          30.0%; Score 6; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PTSSEQ 18
Db 54 PTSSEQ 59

RESULT 8
US-60-425-158-26
; Sequence 26, Application US/60425158
; GENERAL INFORMATION:
; APPLICANT: Rupp, Fabio
; APPLICANT: Wang, Y. Tom
; TITLE OF INVENTION: Methods and Materials Relating to Ly-6-like Polypeptides and
; TITLE OF INVENTION: Polynucleotides
; FILE REFERENCE: HYS-66
; CURRENT APPLICATION NUMBER: US/60/425,158
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 10/245,817
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/323,349
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-425-158-26

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Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-101
; CURRENT APPLICATION NUMBER: US/10/092,411A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5676
; SEQ ID NO 5332
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-5332

Query Match          30.0%; Score 6; DB 6; Length 120;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 PTSSEQ 18
Db 54 PTSSEQ 59

RESULT 8
US-60-425-158-26
; Sequence 26, Application US/60425158
; GENERAL INFORMATION:
; APPLICANT: Rupp, Fabio
; APPLICANT: Wang, Y. Tom
; TITLE OF INVENTION: Methods and Materials Relating to Ly-6-like Polypeptides and
; TITLE OF INVENTION: Polynucleotides
; FILE REFERENCE: HYS-66
; CURRENT APPLICATION NUMBER: US/60/425,158
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 10/245,817
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/323,349
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-425-158-23

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Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GSSEQP 8
Db 79 GSSEQP 84

RESULT 10
US-60-425-158-31
; Sequence 31, Application US/60425158
; GENERAL INFORMATION:
; APPLICANT: Rupp, Fabio
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods and Materials Relating to Ly-6-like Polypeptides and
; TITLE OF INVENTION: Polynucleotides
; FILE REFERENCE: HYS-66
; CURRENT APPLICATION NUMBER: US/60/425,158
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 10/245,817
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/323,349
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/35017
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;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 09/552,317
;; PRIOR FILING DATE: 2000-04-25
;; PRIOR APPLICATION NUMBER: 09/488,725
;; PRIOR FILING DATE: 2000-01-21
;; PRIOR APPLICATION NUMBER: PCT/US01/02623
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: 09/491,404
;; PRIOR FILING DATE: 2000-01-25
;; PRIOR APPLICATION NUMBER: PCT/US01/03800
;; PRIOR FILING DATE: 2001-02-05
;; PRIOR APPLICATION NUMBER: 09/560,875
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: 09/496,914
;; PRIOR FILING DATE: 2000-02-03
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 31
;; LENGTH: 155
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-60-425-158-31

Query Match 30.0%; Score 6; DB 7; Length 155;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GSGEOP 8
Db 58 GSGEOP 63

RESULT 11

US-60-425-158-38
;; Sequence 38, Application US/60425158
;; GENERAL INFORMATION:
;; APPLICANT: Rupp, Fabio
;; APPLICANT: Wang, Zhiwei
;; APPLICANT: Tang, Y. Tom
;; TITLE OF INVENTION: Methods and Materials Relating to Ly-6-like Polypeptides and
;; FILE REFERENCE: HYS-66
;; CURRENT APPLICATION NUMBER: US/60/425,158
;; CURRENT FILING DATE: 2002-11-08
;; PRIOR APPLICATION NUMBER: 10/245,817
;; PRIOR FILING DATE: 2002-09-16
;; PRIOR APPLICATION NUMBER: 60/323,349
;; PRIOR FILING DATE: 2001-09-18
;; PRIOR APPLICATION NUMBER: PCT/US00/35017
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 09/552,317
;; PRIOR FILING DATE: 2000-04-25
;; PRIOR APPLICATION NUMBER: 09/488,725
;; PRIOR FILING DATE: 2000-01-21
;; PRIOR APPLICATION NUMBER: PCT/US01/02623
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: 09/491,404
;; PRIOR FILING DATE: 2000-01-25
;; PRIOR APPLICATION NUMBER: PCT/US01/03800
;; PRIOR FILING DATE: 2001-02-05
;; PRIOR APPLICATION NUMBER: 09/560,875
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: 09/496,914
;; PRIOR FILING DATE: 2000-02-03
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 38
;; LENGTH: 174
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-60-425-158-38

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GSGEOP 8
Db 58 GSGEOP 63

RESULT 12

US-60-425-158-28
;; Sequence 28, Application US/60425158
;; GENERAL INFORMATION:
;; APPLICANT: Rupp, Fabio
;; APPLICANT: Wang, Zhiwei
;; APPLICANT: Tang, Y. Tom
;; TITLE OF INVENTION: Methods and Materials Relating to Ly-6-like Polypeptides and
;; FILE REFERENCE: HYS-66
;; CURRENT APPLICATION NUMBER: US/60/425,158
;; CURRENT FILING DATE: 2002-11-08
;; PRIOR APPLICATION NUMBER: 10/245,817
;; PRIOR FILING DATE: 2002-09-16
;; PRIOR APPLICATION NUMBER: 60/323,349
;; PRIOR FILING DATE: 2001-09-18
;; PRIOR APPLICATION NUMBER: PCT/US00/35017
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;; PRIOR APPLICATION NUMBER: 09/552,317
;; PRIOR FILING DATE: 2000-04-25
;; PRIOR APPLICATION NUMBER: 09/488,725
;; PRIOR FILING DATE: 2000-01-21
;; PRIOR APPLICATION NUMBER: PCT/US01/02623
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: 09/491,404
;; PRIOR FILING DATE: 2000-01-25
;; PRIOR APPLICATION NUMBER: PCT/US01/03800
;; PRIOR FILING DATE: 2001-02-05
;; PRIOR APPLICATION NUMBER: 09/560,875
;; PRIOR FILING DATE: 2000-04-27
;; PRIOR APPLICATION NUMBER: 09/496,914
;; PRIOR FILING DATE: 2000-02-03
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 28
;; LENGTH: 176
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-60-425-158-28

Query Match 30.0%; Score 6; DB 7; Length 176;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GSGEOP 8
Db 79 GSGEOP 84

RESULT 13

US-60-425-158-35
;; Sequence 35, Application US/60425158
;; GENERAL INFORMATION:
;; APPLICANT: Rupp, Fabio
;; APPLICANT: Wang, Zhiwei
;; APPLICANT: Tang, Y. Tom
;; TITLE OF INVENTION: Methods and Materials Relating to Ly-6-like Polypeptides and
;; FILE REFERENCE: HYS-66
;; CURRENT APPLICATION NUMBER: US/60/425,158
;; CURRENT FILING DATE: 2002-11-08
;; PRIOR APPLICATION NUMBER: 10/245,817

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; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/323,349
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/35017
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; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
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; PRIOR FILING DATE: 2000-02-03
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-425-158-35
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; Sequence 49, Application US/60425158
; GENERAL INFORMATION:
; APPLICANT: Rupp, Fabio
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: Methods and Materials Relating to Ly-6-like Polypeptides and
; FILE REFERENCE: HYS-66
; CURRENT APPLICATION NUMBER: US/60/425,158
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: 10/245,817
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/323,349
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
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; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-425-158-49
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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 3 GSGEOP 8
Db 79 GSGEOP 84
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; Sequence 55403, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55403
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-55403
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Db 81 PRGGGP 86
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Job time : 11.7949 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:38:34 : Search time 140 Seconds
(without alignments)
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Title: US-09-876-204-3

Perfect score: 20

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	20	100.0	70	15	US-09-177-315-1
5	20	100.0	70	15	US-09-177-315-5
6	20	100.0	78	1	PCT-US99-24747-3

7	20	100.0	78	1	PCT-US99-24747-7	Sequence 7, Appli
8	20	100.0	78	15	US-09-177-315-3	Sequence 3, Appli
9	20	100.0	78	15	US-09-177-315-7	Sequence 7, Appli
10	20	100.0	131	1	PCT-US99-05359-2	Sequence 2, Appli
11	20	100.0	131	16	US-09-266-465-2	Sequence 2, Appli
12	20	100.0	135	1	PCT-US02-06951-242	Sequence 242, App
13	20	100.0	135	24	US-10-092-750-242	Sequence 242, App
14	20	100.0	143	21	US-09-791-537-52874	Sequence 52874, A
15	20	100.0	143	27	US-60-350-061-261	Sequence 261, App
16	20	100.0	164	21	US-09-791-537-105329	Sequence 105329,
17	20	100.0	192	1	PCT-US98-19765-46	Sequence 46, Appl
18	20	100.0	192	1	PCT-US99-05359-4	Sequence 4, Appli
19	20	100.0	192	1	PCT-US99-24747-12	Sequence 12, Appl
20	20	100.0	192	5	US-08-112-208B-6	Sequence 6, Appli
21	20	100.0	192	5	US-08-160-067-7	Sequence 7, Appli
22	20	100.0	192	6	US-08-248-819-6	Sequence 6, Appli
23	20	100.0	192	7	US-08-320-157-13	Sequence 13, Appl
24	20	100.0	192	8	US-08-470-865-13	Sequence 13, Appl
25	20	100.0	192	8	US-08-483-233-2	Sequence 2, Appli
26	20	100.0	192	8	US-08-483-233-9	Sequence 9, Appli
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33	20	100.0	192	15	US-09-177-315-12	Sequence 12, Appl
34	20	100.0	192	16	US-09-266-465-4	Sequence 4, Appli
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38	20	100.0	192	17	US-09-379-820A-9	Sequence 9, Appli
39	20	100.0	192	18	US-09-456-357-26	Sequence 26, Appl
40	20	100.0	192	19	US-09-587-473-19	Sequence 19, Appl
41	20	100.0	192	20	US-09-617-878-8	Sequence 8, Appli
42	20	100.0	192	20	US-09-633-200-13	Sequence 13, Appl
43	20	100.0	192	20	US-09-693-714-7	Sequence 7, Appli
44	20	100.0	192	21	US-09-791-537-3979	Sequence 3979, Ap
45	20	100.0	192	21	US-09-791-537-127903	Sequence 127903,

ALIGNMENTS

RESULT 1
US-09-876-204-3
: Sequence 3, Application US/09876204
: GENERAL INFORMATION:
: APPLICANT: Gordon C. Shore et al.
: TITLE OF INVENTION: BAX-MEDICATED APOPTOSIS MODULATING
: TITLE OF INVENTION: REAGENTS AND METHODS
: FILE REFERENCE: 50013/011001
: CURRENT APPLICATION NUMBER: US/09/876, 204
: CURRENT FILING DATE: 2001-06-06
: PRIOR APPLICATION NUMBER: 09/166, 028
: PRIOR FILING DATE: 1998-10-05
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-876-204-3

Query Match 100.0%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEOPRGCGPTSSQIM 20
|||||
Db 1 MDGSGEOPRGCGPTSSQIM 20

RESULT 2
PCT-US99-24747-1
; Sequence 1, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-24747-1

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 9.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSSEQIM 20
Db 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 3
PCT-US99-24747-5
; Sequence 5, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-24747-5

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 9.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSSEQIM 20
Db 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 4
US-09-177-315-1
; Sequence 1, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-5756
; CURRENT APPLICATION NUMBER: US/09/177,315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-177-315-1

Query Match
Best Local Similarity 100.0%; Score 20; DB 15; Length 70;

Best Local Similarity 100.0%; Pred. No. 9.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSSEQIM 20
Db 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 5
US-09-177-315-5
; Sequence 5, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-5756
; CURRENT APPLICATION NUMBER: US/09/177,315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-177-315-5

Query Match
Best Local Similarity 100.0%; Score 20; DB 15; Length 70;
Best Local Similarity 100.0%; Pred. No. 9.8e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSSEQIM 20
Db 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 6
PCT-US99-24747-3
; Sequence 3, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-24747-3

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSSEQIM 20
Db 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 7
PCT-US99-24747-7
; Sequence 7, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34


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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-24747-7
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Query Match          100.0%; Score 20; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 MDGSGEQPRGGGPTSSSEQIM 20
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DB 1 MDGSGEQPRGGGPTSSSEQIM 20
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RESULT 8
US-09-177-315-3
; Sequence 3, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-5756
; CURRENT APPLICATION NUMBER: US/09/177,315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-177-315-3
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Query Match          100.0%; Score 20; DB 15; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 MDGSGEQPRGGGPTSSSEQIM 20
|||||
DB 1 MDGSGEQPRGGGPTSSSEQIM 20
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RESULT 9
US-09-177-315-7
; Sequence 7, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX polypeptides
; FILE REFERENCE: 6029-5756
; CURRENT APPLICATION NUMBER: US/09/177,315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-177-315-7
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Query Match          100.0%; Score 20; DB 15; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 MDGSGEQPRGGGPTSSSEQIM 20
|||||
DB 1 MDGSGEQPRGGGPTSSSEQIM 20
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RESULT 10
PCT-US99-05359-2
; Sequence 2, Application PC/TUS9905359
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; GENERAL INFORMATION:
; APPLICANT: MCDONNELL, TIMOTHY J.
; APPLICANT: SWISHER, STEVEN G.
; APPLICANT: FANG, BINGLIANG
; APPLICANT: BRUCKHEIMER, ELIZABETH
; APPLICANT: SARKISS, MONA
; APPLICANT: JI, LIN
; APPLICANT: ROTH, JACK A.
; TITLE OF INVENTION: INDUCTION OF APOPTIC OR CYTOTOXIC GENE EXPRESSION BY
; FILE REFERENCE: INGN:088/INGN:088P
; CURRENT APPLICATION NUMBER: PCT/US99/05359
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: 60/077,541
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Human
PCT-US99-05359-2
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Query Match          100.0%; Score 20; DB 1; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 MDGSGEQPRGGGPTSSSEQIM 20
|||||
DB 1 MDGSGEQPRGGGPTSSSEQIM 20
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RESULT 11
US-09-266-465-2
; Sequence 2, Application US/09266465
; GENERAL INFORMATION:
; APPLICANT: MCDONNELL, TIMOTHY J.
; APPLICANT: SWISHER, STEVEN G.
; APPLICANT: FANG, BINGLIANG
; APPLICANT: BRUCKHEIMER, ELIZABETH
; APPLICANT: SARKISS, MONA
; APPLICANT: JI, LIN
; APPLICANT: ROTH, JACK A.
; TITLE OF INVENTION: INDUCTION OF APOPTIC OR CYTOTOXIC GENE EXPRESSION BY
; FILE REFERENCE: INGN:088/INGN:088P
; CURRENT APPLICATION NUMBER: US/09/266,465
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: 60/077,541
; EARLIER FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Human
US-09-266-465-2
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Query Match          100.0%; Score 20; DB 16; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 MDGSGEQPRGGGPTSSSEQIM 20
|||||
DB 1 MDGSGEQPRGGGPTSSSEQIM 20
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```
RESULT 12
PCT-US02-06951-242
; Sequence 242, Application PC/TUS0206951
; GENERAL INFORMATION:
; APPLICANT: Phyllos, Inc.
; TITLE OF INVENTION: Polypeptides Interactive with BCL-XL
```

FILE REFERENCE: 50036/050W02
CURRENT APPLICATION NUMBER: PCT/US02/06951
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US 60/274,526
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 242
LENGTH: 135
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-06951-242

Query Match 100.0%; Score 20; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGGPTSSSEQIM 20
Db 1 MDGSGEOPRGGPTSSSEQIM 20

RESULT 13
US-10-092-750-242
Sequence 242, Application US/10092750
GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Alpin, Julia
APPLICANT: Wright, Martin C.
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
FILE REFERENCE: 50036/050002
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US 60/274,526
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 242
LENGTH: 135
TYPE: PRT
ORGANISM: Homo sapiens
US-10-092-750-242

Query Match 100.0%; Score 20; DB 24; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGGPTSSSEQIM 20
Db 1 MDGSGEOPRGGPTSSSEQIM 20

RESULT 14
US-09-791-537-52874
Sequence 52874, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Biocomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 52874
LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-537-52874

Query Match 100.0%; Score 20; DB 21; Length 143;

Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGGPTSSSEQIM 20
Db 1 MDGSGEOPRGGPTSSSEQIM 20

RESULT 15
US-60-350-061-261
Sequence 261, Application US/60350061
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS T
TITLE OF INVENTION: INTERACT WITH SRC TYROSINE KINASES AND THE SRC TYROSINE KINAS
FILE REFERENCE: D0185
CURRENT APPLICATION NUMBER: US/60/350,061
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 981
SOFTWARE: PatentIn version 3.0
SEQ ID NO 261
LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
US-60-350-061-261

Query Match 100.0%; Score 20; DB 27; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.9e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGGPTSSSEQIM 20
Db 1 MDGSGEOPRGGPTSSSEQIM 20

Search completed: January 7, 2003, 12:45:31
Job time : 140 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:25:07 : Search time 7.30769 Seconds
(without alignments)
107.838 Million cell updates/sec

Title: US-09-876-204-1
Perfect score: 78
Sequence: 1 MDGSGXXXXXGCPRSSHQI 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	69	88.5	192	1 BAXA_MOUSE	Q07813 mus musculus
2	68	87.2	192	1 BAXA_RAT	Q06390 rattus norv
3	67	85.9	143	1 BAXD_HUMAN	P55269 homo sapien
4	67	85.9	192	1 BAXA_BOVIN	O02703 bos taurus
5	67	85.9	192	1 BAXA_HUMAN	Q07812 homo sapien
6	67	85.9	218	1 BAXB_HUMAN	Q07814 homo sapien
7	46	59.0	654	1 BAXB_HUMAN	Q05944 hydra magni
8	39	50.0	105	1 YGRM_MICRO	P24621 micromonosp
9	38	48.7	334	1 PHP2_SCHPO	P24488 schizosacch
10	38	48.7	487	1 XYL_C_PSEPU	P43503 pseudomonas
11	37	47.4	321	1 ISP_BACCS	P20140 bacillus cl
12	37	47.4	579	1 YH83_SCHPO	Q06502 schizosacch
13	37	47.4	602	1 GAP1_YEAST	P15145 saccharomyc
14	37	47.4	618	1 SPFA_ECOLI	P08395 escherichia
15	37	47.4	631	1 HS73_BOVIN	P34933 bos taurus
16	37	47.4	639	1 HS72_HUMAN	P54652 homo sapien
17	36	46.2	109	1 PER_RHACO	O26231 rhagolellis
18	36	46.2	450	1 SWP1_ENCCU	O9XZV1 encephalito
19	36	46.2	574	1 ME22_SCHPO	O60170 schizosacch
20	36	46.2	862	1 POIG_ECL16H	O66790 echovirus 1
21	36	46.2	1185	1 DRPL_HUMAN	P54259 homo sapien
22	35	44.9	473	1 HN3A_HUMAN	P55317 homo sapien
23	35	44.9	474	1 MERA_STRLI	P30341 streptomyc
24	35	44.9	512	1 GME2_MOUSE	P38929 mus musculu
25	35	44.9	529	1 GME2_RAT	O08873 rattus norv
26	35	44.9	530	1 GME2_HUMAN	O9ukd1 homo sapien
27	35	44.9	633	1 HS72_MOUSE	P17156 mus musculu
28	35	44.9	633	1 HS72_RAT	P16559 rattus norv
29	35	44.9	880	1 TYO3_MOUSE	P55144 mus musculu
30	35	44.9	1709	1 CHD1_HUMAN	O14646 homo sapien
31	34	43.6	154	1 NEU1_CATCO	P15210 catostomus
32	34	43.6	176	1 VLPA_MYCHR	P29228 mycoplasma
33	34	43.6	192	1 COAT_OYMW	P20124 ononis yell

34	34	43.6	347	1	UTR2_YEAST	P32623 saccharomyc
35	34	43.6	351	1	E2B8_HUMAN	P49770 homo sapien
36	34	43.6	359	1	Y199_MYCTU	O07773 mycobacteri
37	34	43.6	370	1	CLCB_PSEPU	P11452 pseudomonas
38	34	43.6	382	1	NDF2_HUMAN	Q15784 homo sapien
39	34	43.6	382	1	NDF2_RAT	O63689 rattus norv
40	34	43.6	383	1	NDF2_MOUSE	O62414 mus musculu
41	34	43.6	384	1	HEM2_DROME	O9V9S8 drosophila
42	34	43.6	401	1	ENO_THENO	O97929 thermoplasm
43	34	43.6	426	1	YF26_MYCTU	O50581 mycobacteri
44	34	43.6	468	1	HN3A_MOUSE	P35582 mus musculu
45	34	43.6	506	1	NPL3_HUMAN	O99457 homo sapien

ALIGNMENTS

```

RESULT 1
BAXA_MOUSE
ID BAXA_MOUSE STANDARD: PRT: 192 AA.
AC 007813:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X DBA/2;
RX MEDLINE=93364978; PubMed=8358790;
RA Olivai Z.N., Millman C.L., Korsmeyer S.J.;
RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
RT accelerates programmed cell death.";
RL Cell 74:609-619(1993).
CC
CC -!- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
CC HOMOLOG E1B 19K PROTEIN, INDUCES THE RELEASE OF CYTOCHROME C,
CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY
CC LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE
CC CESSATION OF SPERM PRODUCTION.
CC
CC -!- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC
CC -!- SUBCELLULAR LOCATION: Membrane-bound.
CC
CC -!- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO
CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
CC SPLICING.
CC
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC
CC -!- DOMAIN: INTACT BAX DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC
CC -!- APOTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC
CC -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L22472; AA03622.1; -.
CC HSSP: P53563; IAF3.
CC MGD: MGI:99702; Bax.
CC InterPro: IPR002475; BCL2_family.
CC InterPro: IPR000712; Bcl2_BH.

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DR Pfam: PF00452; Bcl-2; 1.
 DR SMART: SM00337; BCL; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS0062; BCL2_FAMILY; 1.
 DR APOPTOSIS; Transmembrane; Alternative splicing.
 KW DOMAIN 59 73 BH3.
 FT DOMAIN 98 118 BH1.
 FT DOMAIN 150 165 BH2.
 FT TRANSMEM 172 192 POTENTIAL.
 SQ SEQUENCE 192 AA; 21394 MW; D2E0B3566579FAFF CRC64;
 Query Match
 Best Local Similarity 73.7%; Score 69; DB 1; Length 192;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MDGSGXXXXXGGPTSSQEI 19
 DB 1 MDGSGEQLGSGGPTSSQEI 19
 RESULT 2
 BAXA_RAT STANDARD; PRT; 192 AA.
 ID BAXA_RAT
 AC 063690; Q62995; Q64383;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Apoptosis regulator BAX, membrane isoform alpha.
 GN BAX.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96178771; PubMed=8600029;
 RA Han J., Sabbatini P., Perez D., Rao L., Modha D., White E.;
 RT "The Bcl-2 protein blocks apoptosis by interacting with and
 RT inhibiting the p53-inducible and death-promoting Bax protein.";
 RL Genes Dev. 10:461-477(1996).
 RN [2]
 RP SEQUENCE OF 75-192 FROM N.A.
 RX TISSUE=Brain;
 RC MEDLINE=97147318; PubMed=8994223;
 RA Madison D.L., Pfeiffer S.E.;
 RT "Cloning of the 3' end of rat bax-alpha and corresponding
 RT developmental down-regulation in differentiating primary, cultured
 RT oligodendrocytes.";
 RL Neurosci. Lett. 220:183-186(1996).
 RN [3]
 RP SEQUENCE OF 37-169 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Ovary;
 RX MEDLINE=95129487; PubMed=7828536;
 RA Tilly J.L., Tilly K.L., Kenton M.L., Johnson A.L.;
 RT "Expression of members of the bcl-2 gene family in the immature rat
 RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
 RT cell apoptosis is associated with decreased bax and constitutive
 RT bcl-2 and bcl-x long messenger ribonucleic acid levels.";
 RL Endocrinology 136:232-241(1995).
 CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
 CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
 CC HOMOLOG BCL-2.
 CC ACTIVATION OF CASPASE-3. AND THEREBY APOPTOSIS.
 CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
 CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound.
 CC -1- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO
 CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
 CC HIGHEST LEVELS IN THE TESTIS AND OVARY.

CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAX, BAD AND
 CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
 CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U04929; AAC26327.1; -;
 DR EMBL: U59184; AAC52998.1; -;
 DR EMBL: U32098; AAAT5200.1; -;
 DR EMBL: S76511; AAC60700.2; -;
 DR HSSP: P53563; IAF3.
 DR InterPro: IPR002475; BCL2_family.
 DR InterPro: IPR000712; BCL2_BH.
 DR Pfam: PF00452; Bcl-2; 1.
 DR SMART: SM00337; BCL; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS0062; BCL2_FAMILY; 1.
 DR APOPTOSIS; Transmembrane; Alternative splicing.
 KW DOMAIN 59 73 BH3.
 FT DOMAIN 98 118 BH1.
 FT DOMAIN 150 165 BH2.
 FT TRANSMEM 172 192 POTENTIAL.
 FT CONFLICT 72 72 S -> N (IN REF. 3).
 FT CONFLICT 76 76 L -> M (IN REF. 2).
 FT CONFLICT 126 126 C -> Y (IN REF. 2).
 FT CONFLICT 149 149 L -> F (IN REF. 3).
 FT CONFLICT 159 159 D -> E (IN REF. 1).
 SQ SEQUENCE 192 AA; 21350 MW; 7B3CD198D56DF589 CRC64;
 Query Match
 Best Local Similarity 87.2%; Score 68; DB 1; Length 192;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MDGSGXXXXXGGPTSSQEI 19
 DB 1 MDGSGEQLGSGGPTSSQEI 19
 RESULT 3
 BAXD_HUMAN STANDARD; PRT; 143 AA.
 ID BAXD_HUMAN
 AC P55269;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE BAX protein, cytoplasmic isoform delta.
 GN BAX.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95331797; PubMed=7607685;
 RA Apte S.S., Mattei M.-G., Olsen B.R.;
 RT "Mapping of the human BAX gene to chromosome 19q13.3-q13.4 and
 RT isolation of a novel BAX gene alternatively spliced transcript, BAX delta.";
 RL Genomics 26:592-594(1995).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE

```
CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
CC ALTERNATIVE SPLICING.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U19599; AAC50142.1; -.
CC Genew: HGNC:959; BAX.
CC MIM: 600040; -.
CC DR InterPro: IPR002475; BCL2_family.
CC DR InterPro: IPR000712; BCL2_BH.
CC DR Pfam: PF00452; Bcl-2; 1.
CC DR SMART: SM00337; BCL; 1.
CC DR PROSITE: PS01080; BH1; 1.
CC DR PROSITE: PS01258; BH2; 1.
CC DR PROSITE: PS50062; BCL2_FAMILY; 1.
CC KW Apoptosis; Alternative splicing.
CC FT DOMAIN 49 69 BH1.
CC FT DOMAIN 101 116 BH2.
CC SQ SEQUENCE 143 AA: 15772 MW: BADE4D71D06A75AB CRC64:

Query Match 85.9%; Score 67; DB 1; Length 143;
Best Local Similarity 73.7%; Pred. No. 9.9e-06;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDSGXXXXXGPTSEQI 19
Db 1 MDSGGEOPRGCGPTSEQI 19

RESULT 4
BAXA_BOVIN STANDARD: PRT; 192 AA.
AC 002703;
DT 15-JUL-1999 (Rel. 38; Created)
DT 15-JUL-1999 (Rel. 38; Last sequence update)
DT 15-JUN-2002 (Rel. 41; Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Holstein; TISSUE=Thymus;
RX MEDLINE=98162580; PubMed=9501056;
RA Reyes R.A., Cockrell G.L.;
RT "Increased ratio of bcl-2/dax expression is associated with bovine
RT leukemia virus-induced leukemogenesis in cattle.";
RL Virology 242:184-192(1998).
CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
CC HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY
CC LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE
CC CESSATION OF SPERM PRODUCTION (BY SIMILARITY).
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Membrane-bound (By similarity).
CC -1- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO
CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
CC SPLICING.
CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
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CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
CC EMBL: U92569; AAC48806.1; -.
CC DR HSP: Q07817; 1MA2.
CC DR InterPro: IPR002475; BCL2_family.
CC DR InterPro: IPR000712; BCL2_BH.
CC DR Pfam: PF00452; Bcl-2; 1.
CC DR SMART: SM00337; BCL; 1.
CC DR PROSITE: PS01080; BH1; 1.
CC DR PROSITE: PS01258; BH2; 1.
CC DR PROSITE: PS01259; BH3; 1.
CC DR PROSITE: PS50062; BCL2_FAMILY; 1.
CC KW Apoptosis; Transmembrane; Alternative splicing.
CC FT DOMAIN 59 73 BH3.
CC FT DOMAIN 98 118 BH1.
CC FT DOMAIN 150 165 BH2.
CC FT TRANSMEM 172 192 POTENTIAL.
CC SQ SEQUENCE 192 AA: 21259 MW: 6BAD5B8F1D5F87E CRC64:

Query Match 85.9%; Score 67; DB 1; Length 192;
Best Local Similarity 73.7%; Pred. No. 1.4e-05;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MDSGXXXXXGPTSEQI 19
Db 1 MDSGGEOPRGCGPTSEQI 19

RESULT 5
BAXA_HUMAN STANDARD: PRT; 192 AA.
AC Q07812;
DT 01-FEB-1995 (Rel. 31; Created)
DT 01-FEB-1995 (Rel. 31; Last sequence update)
DT 15-JUN-2002 (Rel. 41; Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=93364978; PubMed=8358790;
RA Oliva J.N., Millman C.L., Korsmeyer S.J.;
RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
RT accelerates programmed cell death.";
RL Cell 74:609-619(1993).
RN [2]
RP MUTAGENESIS, AND FUNCTION OF BH3 DOMAIN.
RX MEDLINE=96091131; PubMed=8521816;
RA Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,
RA Elangovan B., Chinnadurai G., Lutz R.J.;
RT "A conserved domain in Bax, distinct from BH1 and BH2, mediates cell
RT death and protein binding functions.";
RL EMBO J. 14:5589-5596(1995).
RN [3]
RP VARIANT PLASMACYTOMA GLU-11, VARIANT T-CELL ACUTE LYMPHOBLASTIC
```

RP LEUKEMIA ARG-67, AND VARIANT BURKITT LYMPHOMA VAL-108.
 RX MEDLINE-98200607; PubMed-9531611;
 RA Melnick J.P.P., Mensink E.J.B.M., Mang K., Sedlak T.W.,
 RT Sloetjes A.W., de Witte T., Waksman G., Korsmeyer S.J.:
 Hematopoietic malignancies demonstrate loss-of-function mutations of
 BAX.*
 RL Blood 91:2991-2997(1998).
 CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
 CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
 CC HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
 CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.
 CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
 CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound.
 CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
 CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
 CC ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
 CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
 CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
 CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY
 CC -1- DISEASE: Defects in BAX are found in some cell lines from
 CC hematopoietic malignancies as T-cell acute lymphoblastic leukemia,
 CC Burkitt lymphoma, and plasmacytoma.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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 CC -----
 DR EMBL: L22473; AAA03619.1; -.
 DR PIR: A47538; A47538.
 DR HSSP: 007817; 1MAZ.
 DR Genew: HGNC:959; BAX.
 DR MIM: 600040; -.
 DR InterPro: IPR002475; BCL2_family.
 DR InterPro: IPR000712; Bcl2_BH.
 DR Pfam: PF00452; Bcl-2; 1.
 DR SMART: SM00337; BCL; 1.
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR Apoptosis: Anti-oncogene; Transmembrane; Alternative splicing;
 KM Disease mutation.
 FT DOMAIN 59 73 BH3.
 FT 98 118 BH1.
 FT DOMAIN 150 165 BH2.
 FT TRANSMEM 172 192 POTENTIAL.
 FT VARIANT 11 11 G -> E (IN PLASMACYTOMA).
 FT VARIANT 67 67 /FETD-VAR.013575.
 FT G -> R (IN T-CELL ACUTE LYMPHOBLASTIC
 FT LEUKEMIA; LOSS OF HETERODIMERIZATION WITH
 FT BCL-2 OR BCL-X(L)).
 FT /FETD-VAR.007809.
 FT G -> V (IN BURKITT LYMPHOMA; LOSS OF
 FT HOMODIMERIZATION).
 FT /FETD-VAR.013576.
 SQ SEQUENCE 192 AA; 21184 MW; 6C0CDB0A7DE4994 CRC64;
 Query Match Score 67; DB 1; Length 192;
 Best Local Similarity 73.7%; Pred. No. 1.4e-05;
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY, 1 MDGSGXXXXGGPTSSSEQI 19

DB 1 MDGSGEQPRGGGPTSSSEQI 19
 RESULT 6
 BAXB_HUMAN STANDARD; PRT; 218 AA.
 AC 007814;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Apoptosis regulator Bax, cytoplasmic isoform beta.
 GN BAX.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-B-cell;
 RX MEDLINE-93364978; PubMed-8358790;
 RA Oliveira Z.N., Millman C.L., Korsmeyer S.J.:
 RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
 RT accelerates programmed cell death.*".
 RL Cell 74:609-619(1993).
 CC -1- FUNCTION: ACCELERATES PROGRAMMED CELL DEATH BY BINDING TO, AND
 CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
 CC HOMOLOG E1B 19K PROTEIN.
 CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
 CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
 CC CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
 CC ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
 CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
 CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
 CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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 CC -----
 DR EMBL: L22474; AAA03620.1; -.
 DR PIR: B47538; B47538.
 DR HSSP: 007817; 1MAZ.
 DR Genew: HGNC:959; BAX.
 DR MIM: 600040; -.
 DR InterPro: IPR002475; BCL2_family.
 DR InterPro: IPR000712; Bcl2_BH.
 DR Pfam: PF00452; Bcl-2; 1.
 DR SMART: SM00337; BCL; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 DR Apoptosis: Alternative splicing.
 KM Disease mutation.
 FT DOMAIN 59 73 BH3.
 FT 98 118 BH1.
 FT DOMAIN 150 165 BH2.
 SQ SEQUENCE 218 AA; 24220 MW; F69DCD70F960192F CRC64;
 Query Match Score 67; DB 1; Length 218;
 Best Local Similarity 73.7%; Pred. No. 1.6e-05;

XX (UNITW) UNIV WASHINGTON.
 PA Johnson EM, Easton R;
 PI WPI: 2000-339513/29.
 DR Truncated BAX polypeptides useful for preventing apoptosis of neurons
 XX for the treatment of nervous system disorders -
 PT Disclosure: Page 35-36; 43pp; English.
 PS
 XX The present sequence is a human BAX alpha protein, a pro-apoptotic
 CC protein which is a member of BCL-2 family of proteins that are involved
 CC in regulation of neuronal programmed cell death. The patent discloses
 CC specific truncated proteins derived from BAX alpha which inhibit neuronal
 CC apoptosis induced by trophic factor deprivation. The anti-apoptotic
 CC truncated BAX (tBAX) proteins include tBAX70, tBAX78 and their mutants.
 CC These proteins contain the N-terminal region and at least a portion of
 CC the BH3 domain of BAX alpha and lack the BH1, BH2 and C-terminal
 CC transmembrane domains. The tBAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The tBAX proteins are used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.
 XX
 SQ Sequence 192 AA;

Query Match 100.0%; Score 106; DB 21; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDSSGEOPRGCGPTSSSEQIM 20
 DB 1 MDSSGEOPRGCGPTSSSEQIM 20

RESULT 13
 AAY69202
 ID AAY69202 standard; peptide: 192 AA.

AC AAY69202;

DE 30-MAY-2000 (first entry)

XX Amino acid sequence of the human Bax protein.

XX Pro-apoptotic peptide; Bax; BH3 domain; channel inducer; transport;
 KM cytochrome C transport; mitochondria; apoptosis; ion selectivity;
 KM anti-apoptotic BCL-2 family member; neoplasia; Epstein Barr virus;
 KM African swine fever virus; adenovirus; lymphoproliferative condition;
 KM cancer; arthritis; Crohn's disease; inflammation; autoimmune disease;
 KM immunodeficiency; senescence; neurodegenerative disease;
 KM reperfusion cell death; infertility; wound.

OS Homo sapiens.

PN WO200006187-A2.

PD 10-FEB-2000.

PF 30-JUL-1999; 99WO-US17276.

PR 31-JUL-1998; 98US-0127048.

PA (UNITW) UNIV WASHINGTON.

PI Korsmeyer SJ, Schlessinger PH;

WPI: 2000-195193/17.

Modulating apoptosis in cells by modulating channel ion selectivity for
 transport of cytochrome C -

XX Disclosure: Page 34; 57pp; English.
 PS
 XX The present sequence represents the Bax protein. A pro-apoptotic
 CC peptide can be derived from the BH3 domain. The peptide is an inducer
 CC of formation of a channel for transport of cytochrome C out of
 CC mitochondria. The peptide induces apoptosis in a cell. The peptide
 CC changes the ion selectivity of an anti-apoptotic BCL-2 family member
 CC from potassium selective to chloride selective. The specification
 CC also describes inhibitors of apoptosis in cells. The inhibitors and
 CC inducers can be used to treat patients, preferably humans with a
 CC condition mediated by excessive down-regulation of apoptosis,
 CC especially conditions chosen from neoplasias, diseases caused by
 CC Epstein Barr virus, African swine fever virus and adenovirus.
 CC lymphoproliferative conditions, cancer, arthritis, Crohn's disease,
 CC inflammation and autoimmune disease or a condition mediated by
 CC excessive apoptosis, especially immunodeficiency diseases, senescence,
 CC neurodegenerative disease, ischemic and reperfusion cell death,
 CC infertility and wounds. The methods can also be used to identify
 CC apoptosis-modulating compounds.

Query Match 100.0%; Score 106; DB 21; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDSSGEOPRGCGPTSSSEQIM 20
 DB 1 MDSSGEOPRGCGPTSSSEQIM 20

RESULT 14
 AAB74121
 ID AAB74121 standard; Protein: 192 AA.

AC AAB74121;

DE 22-MAY-2001 (first entry)

XX Human bcl-2 associated X protein (Bax) #1.

XX Human; Bax; cytosolic; immunosuppressive; immunostimulant; infection;
 KM apoptosis modulator; bcl-2 associated X protein; cancer therapy; AIDS;
 KM autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;
 KM myocardial infarction; traumatic brain injury; ischaemia;
 KM neurodegenerative diseases; hepatitis; transplant rejection; toxemia;
 KM lymphoproliferative disease.

OS Homo sapiens.

PN US6184202-B1.

PD 06-FEB-2001.

PF 11-SEP-1997; 97US-0927326.

PR 10-NOV-1994; 94US-0337646.

PR 26-AUG-1993; 93US-0112208.

PR 25-MAY-1994; 94US-0248819.

PA (UNITW) UNIV WASHINGTON.

PI Korsmeyer SJ;

WPI: 2001-256104/26.

N-PSDB; AAF77704.

Modulating apoptosis of a cell, useful in maintaining homeostasis in
 adult tissues, or treating proliferative or autoimmune diseases,
 comprises administering a bcl-2 polypeptide that interacts with a 21 KD
 bcl-2 associated X protein -


```
KW Human: Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;
KM bcl-2-related function; apoptosis.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 97..118
FT /note= "BH1 domain"
FT Domain 146..168
FT /note= "BH2 domain"
XX
XX US5856171-A.
XX
XX 10-NOV-1994; 94US-0337646.
XX
XX 10-NOV-1994; 94US-0337646.
XX
XX 26-AUG-1993; 93US-0112208.
XX
XX 25-MAY-1994; 94US-0248819.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Korsmeyer SJ.
XX
XX WPI: 1999-105119/09.
XX
XX N-PSDB; AAV84005.
XX
XX DNA composition encoding bcl-2 two-hybrid and reporter system - for
XX identifying modulators of bcl-2 function
XX
XX Example 1: Columns 71-74: 105pp; English.
XX
XX The present sequence represents a human Bcl-2 associated protein
XX designated Bax. The Bax protein is used in a composition which
XX comprises a bcl-2 family member polypeptide, a naturally occurring
XX Bax polypeptide and an antibody that binds to the Bax polypeptide.
XX The composition is used to identify modulators of bcl-2-related
XX function, e.g. substances that inhibit binding of Bax to bcl-2,
XX which would be potentially useful as drugs for modulating
XX apoptosis.
XX
XX Sequence 192 AA;
SQ
Query Match 100.0%; Score 106; DB 20; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MDGSGEQPRGGGPTSSSEQIM 20
DB 1 MDGSGEQPRGGGPTSSSEQIM 20
RESULT 11
AAW87809
ID AAW87809 standard; Protein; 192 AA.
XX
XX AAW87809;
AC
XX
XX 10-MAR-1999 (first entry)
XX
XX A human Bcl-2 associated protein designated Bax.
XX
XX Human: Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;
XX bcl-2-related function; apoptosis.
XX
XX Homo sapiens.
XX
XX US5856171-A.
XX
XX 05-JAN-1999.
XX
XX 10-NOV-1994; 94US-0337646.
PF
```

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XX
XX 10-NOV-1994; 94US-0337646.
XX
XX 26-AUG-1993; 93US-0112208.
XX
XX 25-MAY-1994; 94US-0248819.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Korsmeyer SJ.
XX
XX WPI: 1999-105119/09.
XX
XX DNA composition encoding bcl-2 two-hybrid and reporter system - for
XX identifying modulators of bcl-2 function
XX
XX Example 7; Fig 7; 105pp; English.
XX
XX The present sequence represents a human Bcl-2 associated protein
XX designated Bax. The Bax protein is used in a composition which
XX comprises a bcl-2 family member polypeptide, a naturally occurring
XX Bax polypeptide and an antibody that binds to the Bax polypeptide.
XX The composition is used to identify modulators of bcl-2-related
XX function, e.g. substances that inhibit binding of Bax to bcl-2,
XX which would be potentially useful as drugs for modulating
XX apoptosis.
XX
XX Sequence 192 AA;
SQ
Query Match 100.0%; Score 106; DB 20; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MDGSGEQPRGGGPTSSSEQIM 20
DB 1 MDGSGEQPRGGGPTSSSEQIM 20
RESULT 12
AAV70827
ID AAV70827 standard; Protein; 192 AA.
XX
XX AAV70827;
AC
XX
XX 31-JUL-2000 (first entry)
XX
XX Human BAX alpha protein.
XX
XX Human: truncated BAX protein; tBAX; BAX alpha; BCL-2 family; head trauma;
XX neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
XX apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
XX spinal cord injury; stroke; pro-apoptotic; PCD; programmed cell death.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 1..58
XX FT /label= N-terminal_region
XX FT 59..73
XX FT /label= BH3_domain
XX FT /note= "BCL-2 Homology domain 3"
XX FT 98..118
XX FT /label= BH1_domain
XX FT 150..165
XX FT /label= BH2_domain
XX FT 169..188
XX FT /label= Transmembrane_domain
XX
XX WO200023083-A1.
XX
XX 27-APR-2000.
XX
XX 22-OCT-1999; 99WO-US24747.
XX
XX 22-OCT-1998; 98US-0177315.
PF
```

OY 1 MDSCGEOPRGCGPTSSSEQIM 20
 ||||||||||||||||
 Db 1 MDSCGEOPRGCGPTSSSEQIM 20

RESULT 8
 AAY34150
 ID AAY34150 standard; Protein; 192 AA.
 AC AAY34150:
 XX
 DT 30-NOV-1999 (first entry)
 XX
 DE Human wild-type Bax protein.
 XX
 KW Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 59..101 "Portion of BH3 domain essential for dimerisation"
 XX
 FT /note="Portion of BH3 domain essential for dimerisation"
 XX
 PN WO946371-A2.
 XX
 PD 16-SEP-1999.
 XX
 PF 11-MAR-1999; 99MO-US05359.
 XX
 PR 11-MAR-1998; 98US-0077541.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI McDonnell TJ, Swisher SG, Fang B, Bruckheimer EM, Sarkiss MG;
 PI Ji L, Roth JA;
 XX
 DR WPI: 1999-551404/46.
 DR N-PSDB; AA219764.
 XX
 PT New adenovirus vectors, used for killing or inhibiting the growth of
 PT cells and for treating cancers -
 XX
 PS Disclosure; Page 149-150; 151pp; English.
 XX
 CC This sequence represents human wild-type Bax protein. A naturally
 CC occurring mutant protein (AAY34149) was also isolated. Bax (Bcl-2
 CC associated x protein) is a proapoptotic member of the Bcl-2 gene family.
 CC Bax functions as a primary response gene in the p53-regulated apoptotic
 CC pathway. The Bax gene promoter has 4 p53 binding sites and the
 CC expression of Bax is upregulated at the transcriptional level by p53, and
 CC Bax mRNA and protein expression have been shown to increase following
 CC induction of p53. Bax protein can function as a homodimer, or it can
 CC heterodimerise with other Bcl-2 gene family members such as the
 CC antiapoptotic protein Bcl-2. Heterodimerisation of Bcl-2 family members
 CC provides a means of controlling cell death via the "rheostat" model. This
 CC model suggests that the relative amounts of Bcl-2 and Bax determine the
 CC susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess,
 CC Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is
 CC in excess, however, Bax homodimers predominate and the cell becomes
 CC susceptible to apoptosis following exposure to an apoptotic stimulus.
 CC Additionally, Bax can function in its monomeric form to accelerate cell
 CC death. Use of novel adenoviral vectors containing the Bax gene may
 CC augment and complement wild-type p53 gene therapy, which induces a G1
 CC cell cycle arrest and/or apoptosis in malignant cells carrying p53
 CC mutations. In addition, Bax overexpression could provide the apoptotic
 CC effect of p53 without the need for p53 itself.
 XX
 SQ Sequence 192 AA;

Query Match 100.0%; Score 106; DB 20; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDSCGEOPRGCGPTSSSEQIM 20
 ||||||||||||||||
 Db 1 MDSCGEOPRGCGPTSSSEQIM 20

RESULT 9
 AAY05435
 ID AAY05435 standard; peptide; 192 AA.
 AC AAY05435:
 XX
 DT 02-JUL-1999 (first entry)
 XX
 DE Human BAX protein sequence.
 XX
 KW BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;
 KW apoptosis promoter; cancer cell; virus infected cell; inflammation;
 KW autoantibody producing cell; cancer; lymphoproliferative condition;
 KW arthritis; autoimmune disease; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO916787-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 22-SEP-1998; 98MO-US19765.
 XX
 PR 07-OCT-1997; 97US-0946039.
 PR 26-SEP-1997; 97US-0060133.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ;
 PI
 XX
 DR WPI: 1999-255058/21.
 DR
 XX
 PT Bcl homology domain 3 polypeptide
 PT
 XX
 PS Disclosure; Fig 21c; 104pp; English.
 XX
 CC This sequence represents the human BAX protein.
 CC The invention relates to a bcl homology domain 3 (BH3 domain),
 CC derived from a proapoptotic member of the BCL-2 family. The
 CC BH3 polypeptide can be used in a method for promoting apoptosis in a
 CC target cell, especially where the cell is a cancer cell, a virus infected
 CC cell or an autoantibody producing cell. The BH3 polypeptide can be used
 CC in therapeutic compositions for treating disease including cancer, other
 CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
 CC diseases, which may result from the down regulation of cell death
 CC regulation.
 XX
 SQ Sequence 192 AA;

Query Match 100.0%; Score 106; DB 20; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAV34149
 ID AAV34149 standard; Protein: 131 AA.
 AC AAV34149;
 DT 30-NOV-1999 (first entry)
 DE Human truncated Bax protein.
 XX
 KM Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 59..101
 FT /note="Portion of BH3 domain essential for dimerisation"
 XX
 PN W09946371-A2.
 XX
 PD 16-SEP-1999.
 XX
 PF 11-MAR-1999; 99WO-US05359.
 XX
 PR 11-MAR-1998; 98US-0077541.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI McDonnell TJ, Swisher SG, Fang B, Bruckheimer EM, Sarkiss MG;
 PI Ji L, Roth JA;
 DR WPI: 1999-551404/46.
 DR N-PSDB: AA219763.
 XX
 PT New adenovirus vectors, used for killing or inhibiting the growth of
 PT cells and for treating cancers -
 PS
 PS Claim 26; Page 148-149; 151pp: English.
 XX
 CC This sequence represents a human truncated Bax protein. The cDNA
 CC contains a single base deletion relative to the wild-type (AA219764),
 CC causing a frameshift which leads to translation of a premature stop
 CC codon, resulting in a truncated protein. However, the domain responsible
 CC for its function is still present in the truncated protein. Bax (Bcl-2
 CC associated X protein) is a proapoptotic member of the Bcl-2 gene family.
 CC Bax functions as a primary response gene in the p53-regulated apoptotic
 CC pathway. The Bax gene promoter has 4 p53 binding sites and the
 CC expression of Bax is upregulated at the transcriptional level by p53, and
 CC Bax mRNA and protein expression have been shown to increase following
 CC induction of p53. Bax protein can function as a homodimer, or it can
 CC heterodimerise with other Bcl-2 gene family members such as the
 CC antiapoptotic protein Bcl-2. Heterodimerisation of Bcl-2 family members
 CC provides a means of controlling cell death via the "rheostat" model. This
 CC model suggests that the relative amounts of Bcl-2 and Bax determine the
 CC susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess,
 CC Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is
 CC in excess, however, Bax homodimers predominate and the cell becomes
 CC susceptible to apoptosis following exposure to an apoptotic stimulus.
 CC Additionally, Bax can function in its monomeric form to accelerate cell
 CC death. Use of novel adenoviral vectors containing this Bax gene may
 CC augment and complement wild-type p53 gene therapy, which induces a G1
 CC cell cycle arrest and/or apoptosis in malignant cells carrying p53
 CC mutations. In addition, Bax overexpression could provide the apoptotic
 CC effect of p53 without the need for p53 itself.
 CC
 XX
 SQ Sequence 131 AA;

Query Match 100.0%; Score 106; DB 20; Length 131;
 Best Local Similarity 100.0%; Pred. No. 1.1e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEOPRGCGPTSSFOIM 20
 I|||||I|||||I|||||I|||||I
 DB 1 MDGSGEQPRGCGPTSSFOIM 20

RESULT 7
 AAR71406
 ID AAR71406 standard; Protein: 192 AA.
 AC AAR71406;
 DT 15-NOV-1995 (first entry)
 DE Human Bax protein.
 XX
 KM Human: bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line;
 KM apoptosis; membrane-associated cytoplasmic protein; B cell; T cell;
 KM proliferation; cell cycle progression; Bax; apoptotic cell death;
 KM apoptosis; cytokine; death repressor; BH1; BH2; cancer therapy;
 KM hyperplasia; immunodeficiency disease; AIDS; neurodegeneration;
 KM ischaemic cell death.
 XX
 OS Homo sapiens.
 XX
 PN W09505750-A.
 XX
 PD 02-MAR-1995.
 XX
 PF 24-AUG-1994; 94WO-US09701.
 XX
 PR 26-AUG-1993; 93US-0112208.
 PR 25-MAY-1994; 94US-0248819.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Korsmeyer SJ;
 PI WPI: 1995-106605/14.
 DR N-PSDB: AAQ97606.
 XX
 PT Methods for producing and identifying mutant bcl-2 proteins -
 PT that lack death repressor activity and/or lacks binding to Bax.
 PS
 PS Disclosure; Fig 3; 133pp: English.
 XX
 CC This sequence represents human Bax protein. Bax is a protein which is
 CC associated with the human bcl-2 alpha and beta proteins, the sequences
 CC of which are given in AAR71404-05 respectively. bcl-2 is encoded by a
 CC proto-oncogene and is capable of inhibiting apoptosis in many
 CC hematopoietic cell systems. bcl-2 is a 26 kD membrane-associated
 CC cytoplasmic protein and is thought to function by enhancing the survival
 CC of hematopoietic cells of B and T origins rather than directly promoting
 CC proliferation of these cell types. bcl-2 has not been shown to directly
 CC promote cell cycle progression nor does it necessarily alter the dose
 CC response to limiting concentrations of IL-3. bcl-2 has been shown to
 CC form heterodimers with this 21 kD protein, Bax. Overexpressed Bax
 CC accelerates apoptotic cell death induced by cytokine deprivation in an
 CC IL-3 dependent cell line, and it also acts to counter the death repressor
 CC activity of bcl-2. Therefore, the ratio between bcl-2 and Bax determines
 CC cell survival or death following an apoptotic stimulus. The invention
 CC gives a mutant form of bcl-2 in which there is at least one amino acid
 CC substitution or deletion in the BH1 or BH2 domains. This makes the
 CC mutant protein substantially incapable of binding Bax and/or incapable
 CC of death repressor activity. Down regulation of bcl-2 is useful in
 CC cancer therapy, controlling hyperplasias and eliminating self-reactive
 CC clones in autoimmunity by favouring death effector molecules. Up
 CC regulating bcl-2 is beneficial in treatment and diagnosis of immuno-
 CC deficiency diseases, including AIDS and neurodegenerative and ischaemic
 CC cell death.
 CC
 XX
 SQ Sequence 192 AA;

Query Match 100.0%; Score 106; DB 16; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.6e-07;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
XX SO Sequence 70 AA;
Query Match 100.0%; Score 106; DB 21; Length 70;
Best Local Similarity 100.0%; Pred. No. 5.6e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSSGEOPRGCGPTSSBOIM 20
   |||
Db 1 MDSSGEOPRGCGPTSSBOIM 20

RESULT 4
AA70818
ID AAY70818 standard; protein; 78 AA.
AC AAY70818;
XX
XX 31-JUL-2000 (first entry)
DE Human neuroprotective truncated BAX protein, tBAX78.
XX
XX Human; truncated BAX protein; tBAX78; BAX alpha; BCL-2 family;
XX neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
XX apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
XX spinal cord injury; head trauma; stroke.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT Region 1..58
FT /note= "N-terminal region of BAX alpha"
FT Domain 59..73
FT /label= BH3_domain
XX
XX WO200023083-A1.
XX
XX 27-APR-2000.
XX
XX 22-OCT-1999; 99WO-US24747.
XX
XX 22-OCT-1998; 98US-0177315.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Johnson EM, Easton R;
XX
XX WPI: 2000-339513/29.
XX
XX Truncated BAX polypeptides useful for preventing apoptosis of neurons
XX for the treatment of nervous system disorders -
XX
XX Claim 4; Page 33; 43pp; English.
XX
XX The present sequence is a specifically claimed truncated BAX protein
XX tBAX78 which inhibits neuronal apoptosis induced by trophic factor
XX deprivation. The protein consists of first 78 amino acids of human
XX BAX alpha, that includes the N-terminal region and BH3
XX domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of
XX the full-length BAX alpha. The tBAX protein lacking only the
XX transmembrane domain has been shown to have anti-apoptotic activity.
XX The present sequence is used to treat diseases associated with neuronal
XX apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
XX spinal cord injury, head trauma and stroke.
XX
XX Sequence 78 AA;

Query Match 100.0%; Score 106; DB 21; Length 78;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSSGEOPRGCGPTSSBOIM 20
   |||
Db 1 MDSSGEOPRGCGPTSSBOIM 20
```

```
Db 1 MDSSGEOPRGCGPTSSBOIM 20

RESULT 5
AA70822
ID AAY70822 standard; protein; 78 AA.
XX
XX AAY70822;
XX
XX 31-JUL-2000 (first entry)
DE Human neuroprotective truncated BAX protein tBAX78 mutant.
XX
XX Human; truncated BAX protein; tBAX78M; BAX alpha; BCL-2 family; mutant;
XX neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
XX apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
XX spinal cord injury; head trauma; stroke.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
FH Key Location/Qualifiers
FT Misc-difference 55
FT /note= "Wild type Ser is substituted by Ala"
FT Misc-difference 60
FT /note= "Wild type Ser is substituted by Ala"
FT Region 71..78
FT /note= "sequence not found in BAX alpha"
XX
XX WO200023083-A1.
XX
XX 27-APR-2000.
XX
XX 22-OCT-1999; 99WO-US24747.
XX
XX 22-OCT-1998; 98US-0177315.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Johnson EM, Easton R;
XX
XX WPI: 2000-339513/29.
XX
XX N-PSDB; AAD00125.
XX
XX Truncated BAX polypeptides useful for preventing apoptosis of neurons
XX for the treatment of nervous system disorders -
XX
XX Claim 4; Page 34; 43pp; English.
XX
XX The present sequence is a specifically claimed truncated BAX protein,
XX tBAX78 mutant (tBAX78M) which inhibits neuronal apoptosis induced by
XX trophic factor deprivation. The protein consists of the N-terminal
XX region and a portion of BH3 domain of human BAX alpha, and a novel
XX C-terminal sequence of 8 amino acids not present in BAX alpha.
XX It lacks the BH1, BH2 and C-terminal transmembrane
XX domains of the full-length BAX alpha. The tBAX protein lacking only the
XX transmembrane domain has been shown to have anti-apoptotic activity.
XX The present sequence is used to treat diseases associated with neuronal
XX apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
XX spinal cord injury, head trauma and stroke.
XX
XX Sequence 78 AA;

Query Match 100.0%; Score 106; DB 21; Length 78;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSSGEOPRGCGPTSSBOIM 20
   |||
Db 1 MDSSGEOPRGCGPTSSBOIM 20

RESULT 6
```

XX The present invention describes a pure protein (P1) comprising a BAX
 CC polypeptide lacking an apoptotic regulation of targeting (ART) domain.
 CC P1 has cytostatic activity and can be used in the modulation of
 CC apoptosis. The polypeptides and methods from the present invention are
 CC useful for identifying compounds that modulate apoptosis which can then
 CC be used for treating cancer. The present sequence represents a human
 CC BAX peptide sequence of amino acids 1 to 20, which is used in an
 CC example from the present invention.

XX Sequence 20 AA;

Query Match 100.0%; Score 106; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGCGPTSSFOIM 20
 DB 1 MDGSGEOPRGCGPTSSFOIM 20

RESULT 2

AA70816
 ID AAY70816 standard; Protein: 70 AA.

XX AAY70816;

DT 31-JUL-2000 (first entry)

DE Human neuroprotective truncated BAX protein, tBAX70.

XX Human: truncated BAX protein; tBAX70; BAX alpha; BCL-2 family;

KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;

KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;

KW spinal cord injury; head trauma; stroke.

XX Homo sapiens.

OS Location/Qualifiers

XX Key

XX Region

XX Domain

XX

XX

XX

XX

XX

XX

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XX

XX

XX

XX

XX

XX

XX

Claim 4; Page 32; 43pp; English.

Truncated BAX polypeptides useful for preventing apoptosis of neurons
 for the treatment of nervous system disorders -

WPI; 2000-339513/29.

Johnson EM, Easton R;

(UNITW) UNIV WASHINGTON.

22-OCT-1998; 98US-0177315.

22-OCT-1999; 99WO-US24747.

27-APR-2000.

WO200023083-A1.

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XX

CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.

XX Sequence 70 AA;

Query Match 100.0%; Score 106; DB 21; Length 70;
 Best Local Similarity 100.0%; Pred. No. 5.6e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGCGPTSSFOIM 20
 DB 1 MDGSGEOPRGCGPTSSFOIM 20

RESULT 3

AA70820
 ID AAY70820 standard; Protein: 70 AA.

XX AAY70820;

DT 31-JUL-2000 (first entry)

DE Human neuroprotective truncated BAX protein tBAX70 mutant.

XX Human: truncated BAX protein; tBAX70M; BAX alpha; BCL-2 family; mutant;

KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;

KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;

XX Homo sapiens.

OS Synthetic.

XX Key

XX Region

XX Domain

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Claim 4; Page 33-34; 43pp; English.

Truncated BAX polypeptides useful for preventing apoptosis of neurons
 for the treatment of nervous system disorders -

WPI; 2000-339513/29.

Johnson EM, Easton R;

(UNITW) UNIV WASHINGTON.

22-OCT-1998; 98US-0177315.

22-OCT-1999; 99WO-US24747.

27-APR-2000.

WO200023083-A1.

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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:24:47 : Search time 31.7949 Seconds
(without alignments)
83.819 Million cell updates/sec

Title: US-09-876-204-3
Perfect score: 106
Sequence: 1 MDGSGEPRGCGPTSSQIM 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	100.0	20	21	AAV90736 Human BAX amino ac
2	106	100.0	70	21	AAV70816 Human neuroprotect
3	106	100.0	70	21	AAV70820 Human neuroprotect
4	106	100.0	78	21	AAV70818 Human neuroprotect
5	106	100.0	78	21	AAV70822 Human neuroprotect
6	106	100.0	131	20	AAV34149 Human truncated Ba
7	106	100.0	192	16	AAV71406 Human Bax protein.
8	106	100.0	192	20	AAV34150 Human wild-type Ba
9	106	100.0	192	20	AAV05435 Human BAX protein
10	106	100.0	192	20	AAW87804 A human Bcl-2 asso

11	106	100.0	192	20	AAW87809 A human Bcl-2 asso
12	106	100.0	192	21	AAV70827 Human BAX alpha pr
13	106	100.0	192	21	AAV69202 Amino acid sequenc
14	106	100.0	192	22	AAW74121 Human bcl-2 associ
15	106	100.0	192	22	AAW74126 Human bcl-2 associ
16	106	100.0	192	22	AAW48286 Human Bax protein.
17	106	100.0	192	22	AAW35129 Human Bax. Homo s
18	106	100.0	192	22	AAW50539 Human Bax protein
19	106	100.0	192	23	AAV76552 Human Bax polypept
20	106	100.0	221	18	AAW10688 Bax omega protein,
21	103	97.2	331	20	AAV39263 Coding region of c
22	101	95.3	197	21	AAV78512 Truncated Bax amin
23	83	78.3	20	21	AAV90737 Mouse BAX amino ac
24	83	78.3	70	21	AAV70817 Mouse neuroprotect
25	83	78.3	70	21	AAV70821 Mouse neuroprotect
26	83	78.3	78	21	AAV70819 Mouse neuroprotect
27	83	78.3	78	21	AAV70823 Mouse neuroprotect
28	83	78.3	192	16	AAW71407 Murine Bax protein
29	83	78.3	192	20	AAW05434 Murine Bcl-2 associ
30	83	78.3	192	20	AAW87805 Murine Bcl-2 associ
31	83	78.3	192	20	AAW87808 Murine Bcl-2 associ
32	83	78.3	192	21	AAV70828 Mouse BAX alpha pr
33	83	78.3	192	22	AAW74122 Murine bcl-2 assoc
34	83	78.3	192	22	AAW74125 Murine bcl-2 assoc
35	83	78.3	192	22	AAW35128 Murine Bax. Mus s
36	83	78.3	192	23	AAV76551 Rat BAX amino acid
37	81	76.4	20	21	AAV90738 Apoptotic regulati
38	67	63.2	19	21	AAV90735 A bcl-2 associated
39	65	61.3	41	20	AAW87807 N-terminus of Baxg
40	65	61.3	41	22	AAW74124 Human protein kina
41	49.5	46.7	794	22	AAU03517 Human kinase PKIN-
42	49.5	46.7	794	23	AAE16271 Human purified sec
43	48	45.3	116	22	AAW69496 Human polypeptide
44	48	45.3	196	22	AAW40686 Human protein seq
45	47.5	44.8	531	22	AAW78938

ALIGNMENTS

RESULT 1

AAV90736
ID AAV90736 standard; peptide: 20 AA.
XX
AC AAV90736;
XX
DT 17-RNG-2000 (first entry)
XX
DE Human BAX amino acid sequence 1 to 20 SEQ ID NO:2.
XX
KW Apoptotic regulation of targeting domain; ART domain; BAX; apoptosis;
KW cell death; cancer; cytostatic.
XX
OS Homo sapiens.
XX
PN WO200020446-A2.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-1B01680.
XX
PR 05-OCT-1998; 98US-0166028.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Shore GC, Goping S;
XX
DR WPI; 2000-303740/26.
XX
PT BAX polypeptide lacking an ART domain, useful for identifying agents
XX that modulate apoptosis which can then be used for treating cancer -
XX
PS Example 2; Page 52; 53pp; English.

```

; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5425
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-5425

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Query Match          38.7%; Score 41; DB 10; Length 322;
Best Local Similarity 37.5%; Pred. No. 1,3e+02;
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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OY 5 GEOPRGCGPTSSQIM 20
    1 111 11 ::::
Db 250 GHVORCGSPTGADRVL 265

```

Search completed: January 7, 2003, 12:37:21
 Job time : 7.69231 secs

Sequence 2, Application US/09854093
Patent No. US20020151698A1
GENERAL INFORMATION:
APPLICANT: Lester, Henry A.
Dascal, Nathan
Lim, Nancy
Schreibmayer, Wolfgang
Davidson, No. US20020151698A1man
TITLE OF INVENTION: DNA ENCODING INWARD RECTIFIER, G-PROTEIN
ACTIVATED, MAMMALIAN PORRASSIUM KGA
CHANNEL AND USES THEREOF
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fleht Hohbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,093
FILING DATE: 10-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/904,234
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Vance, Dolly A.
REGISTRATION NUMBER: 39,054
REFERENCE/DOCKET NUMBER: A-55891-1/RFT/DAV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-854-093-2
Query Match 39.6%; Score 42; DB 10; Length 501;
Best Local Similarity 44.4%; Pred. No. 1.5e+02;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 3 GSGEPRGGGPTSSQIM 20
DB 21 GSGLPQGGPQGPQDLY 38
RESULT 14
US-09-864-761-45406
Sequence 45406, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 45406
LENGTH: 24
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007164.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.59
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.93
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.82
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.89
US-09-864-761-45406
Query Match 38.7%; Score 41; DB 10; Length 24;
Best Local Similarity 58.3%; Pred. No. 10;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 MDGSGEPRGGG 12
DB 13 VECGSEPRVKCGG 24
RESULT 15
US-09-815-242-5425
Sequence 5425, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
Prokaryotes

Query Match 41.5%; Score 44; DB 10; Length 41;
Best Local Similarity 47.1%; Pred. No. 6.9;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 2 DSGEOPRGCGPTSE01 18
||| ||| |
Db 4 DGECEEGGGGKKKEE 20

RESULT 10

US-10-058-820-5
; Sequence 5, Application US/10058820
; Patent No. US2002015479A1
; GENERAL INFORMATION:
; APPLICANT: Bogan, Jonathan S.
; TITLE OF INVENTION: Expression Cloning Method
; FILE REFERENCE: 0399.2025-002
; CURRENT APPLICATION NUMBER: US/10/058,820
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/325,651
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/298,963
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/264,816
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-058-820-5

Query Match 41.5%; Score 44; DB 9; Length 441;
Best Local Similarity 57.1%; Pred. No. 73;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 6 EOPRGCGPTSE01 19
||| ||| |
Db 66 KOPRARGPTSD0S1 79

RESULT 11

US-09-738-626-5681
; Sequence 5681, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, MAKIO
; APPLICANT: SENOHI, AKIHITO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5681
; LENGTH: 534

TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5681

Query Match 40.6%; Score 43; DB 9; Length 534;
Best Local Similarity 61.5%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGCGP 13
||| ||| |
Db 195 MDARFENPIGNP 207

RESULT 12

US-09-039-927A-2
; Sequence 2, Application US/09039927A
; Patent No. US20020052018A1
; GENERAL INFORMATION:
; APPLICANT: Lester, Henry A.
; Davidson, No. US20020052018A1man
; Kofuji, Paulo
; TITLE OF INVENTION: INWARD RECTIFIER, G-PROTEIN ACTIVATED,
; MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Flehr Hobach Test Albritton & Herbert LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,927A
; FILING DATE: 16-Mar-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/066,371
; FILING DATE: 21-MAR-1993
; APPLICATION NUMBER: US 08/614,801
; FILING DATE: 07-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Treccartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-63098-1/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-039-927A-2

Query Match 39.6%; Score 42; DB 10; Length 501;
Best Local Similarity 44.4%; Pred. No. 1.5e+02;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 3 GSGEOPRGCGPTSE01M 20
||| ||| |
Db 21 GSGIQPGGPGGPGQQLV 38

RESULT 13

US-09-854-093-2

US-09-925-301-1634

Query Match 42.5%; Score 45; DB 10; Length 88;

Best Local Similarity 57.1%; Pred. No. 11;

Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 GSGEOPRGCGPTS 16

Db 17 GASAPRGCGPARS 30

RESULT 1

US-09-925-299-911

Sequence 911, Application US/09925299

Patent No. US20020055627A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA102

CURRENT APPLICATION NUMBER: US/09/925,299

CURRENT FILING DATE: 2000-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05883

PRIOR FILING DATE: 2000-08-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-08-12

NUMBER OF SEQ ID NOS: 155

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 911

LENGTH: 1242

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (224)

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (1013)

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (1034)

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

US-09-925-299-911

Query Match 42.5%; Score 45; DB 10; Length 1242;

Best Local Similarity 60.0%; Pred. No. 1.5e+02;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 DSGGEOPRGCGPTS 16

Db 1097 ECGSEGRSGSOS 1111

RESULT 8

US-09-119-855-11

Sequence 11, Application US/09119855

Patent No. US20020099197A1

GENERAL INFORMATION:

APPLICANT: Curtis, Roy A.J.

TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

FILE REFERENCE: mnl-055

CURRENT APPLICATION NUMBER: US/09/119,855

CURRENT FILING DATE: 1998-07-21

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 11

LENGTH: 1284

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-119-855-11

Query Match

Best Local Similarity 42.5%; Score 45; DB 10; Length 1284;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 GSGEOPRGCGPTS 15

Db 760 GKGEKNGGCPSS 772

RESULT 9

US-09-864-761-38626

Sequence 38626, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: Aeomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263,6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 38626

LENGTH: 41

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AC000053.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1

US-09-864-761-38626

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; TITLE OF INVENTION: SPECIFICITY AND APOPTOSIS-INDUCING ACTIVITIES
; FILE REFERENCE: 9457-009-999
; CURRENT APPLICATION NUMBER: US/09/033,525
; CURRENT FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-033-525-2
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```

Query Match
Best Local Similarity 97.2%; Score 103; DB 10; Length 331;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MDGSGEQPRGGPTSSSEQIM 20
Db 140 LDGSGEQPRGGPTSSSEQIM 159
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RESULT 3
US-09-876-204-4
; Sequence 4, Application US/09876204
; Patent No. US20020052316A1
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/876,204
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/166,028
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-876-204-4
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Query Match
Best Local Similarity 78.3%; Score 83; DB 10; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 MDGSGEQPRGGPTSSSEQIM 20
Db 1 MDGSGEQDLGSGGPTSSSEQIM 20
```

```

RESULT 4
US-09-876-204-5
; Sequence 5, Application US/09876204
; Patent No. US20020052316A1
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/876,204
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/166,028
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-876-204-5
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Query Match
Best Local Similarity 76.4%; Score 81; DB 10; Length 20;
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Best Local Similarity 80.0%; Pred. No. 4.2e-05;
Matches 16; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 1 MDGSGEQPRGGPTSSSEQIM 20
Db 1 MDGSGDHLGGCGPTSSSEQIM 20
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```

RESULT 5
US-09-876-204-1
; Sequence 1, Application US/09876204
; Patent No. US20020052316A1
; GENERAL INFORMATION:
; APPLICANT: Gordon C. Shore et al.
; TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
; FILE REFERENCE: 50013/011001
; CURRENT APPLICATION NUMBER: US/09/876,204
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/166,028
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic based on consensus sequence of Homo
; OTHER INFORMATION: sapiens, Mus musculus, and Rattus norvegicus
; NAME/KEY: VARIANT
; LOCATION: (6)...(10)
; OTHER INFORMATION: Xaa at 6 can be E or D; Xaa at 7 can be Q or H;
; OTHER INFORMATION: Xaa at 8 can be L or P; Xaa at 9 can be R or G;
; OTHER INFORMATION: Xaa at 10 can be S or G;
US-09-876-204-1
```

```

Query Match
Best Local Similarity 63.2%; Score 67; DB 10; Length 19;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 1 MDGSGEQPRGGPTSSSEQI 19
Db 1 MDGSGXXXXXGGPTSSSEQI 19
```

```

RESULT 6
US-09-925-301-1634
; Sequence 1634, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1634
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (82)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (88)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:30:53 : Search time 7.69231 Seconds
(without alignments)
49.274 Million cell updates/sec

Title: US-09-876-204-3
Perfect score: 106
Sequence: 1 MDGSGEOPRGCGPTSSSEQIM 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: PublishedApplications_AA.*
2: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCITUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NBW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	100.0	20	US-09-876-204-3	Sequence 3, Appl1
2	103	97.2	331	US-09-033-525-2	Sequence 2, Appl1
3	83	78.3	20	US-09-876-204-4	Sequence 4, Appl1
4	81	76.4	20	US-09-876-204-5	Sequence 5, Appl1
5	67	63.2	19	US-09-876-204-1	Sequence 1, Appl1
6	45	42.5	88	US-09-925-301-1634	Sequence 1634, Ap
7	45	42.5	1242	US-09-925-299-911	Sequence 911, App
8	45	42.5	1284	US-09-119-855-11	Sequence 11, Appl
9	44	41.5	41	US-09-864-761-38626	Sequence 38626, A
10	44	41.5	441	US-10-058-820-5	Sequence 5, Appl1
11	43	40.6	534	US-09-738-626-5661	Sequence 5681, Ap
12	42	39.6	501	US-09-039-927A-2	Sequence 2, Appl1
13	42	39.6	501	US-09-854-093-2	Sequence 2, Appl1
14	41	38.7	24	US-09-864-761-45406	Sequence 45406, A
15	41	38.7	322	US-09-815-242-5425	Sequence 5425, Ap
16	41	38.7	322	US-09-815-242-12619	Sequence 12619, Ap
17	41	38.7	322	US-09-815-242-12907	Sequence 12907, A
18	41	38.7	351	US-09-350-874-61	Sequence 61, Appl
19	41	38.7	790	US-09-801-368-184	Sequence 184, App

20	41	38.7	1329	10	US-09-815-242-10112	Sequence 10112, A
21	41	38.7	1362	10	US-09-815-242-14009	Sequence 14009, A
22	40.5	38.2	124	10	US-09-995-494-67	Sequence 97, Appl
23	40.5	38.2	127	10	US-09-925-300-1838	Sequence 1838, Ap
24	40.5	38.2	142	9	US-09-984-245-230	Sequence 230, App
25	40.5	38.2	150	10	US-09-925-300-1433	Sequence 1433, Ap
26	40.5	38.2	218	9	US-10-067-813-17	Sequence 17, Appl
27	40.5	38.2	840	9	US-10-025-880-1102	Sequence 1102, Ap
28	40.5	38.2	840	10	US-09-922-217-1102	Sequence 1102, Ap
29	40	37.7	135	9	US-09-796-692-2384	Sequence 2384, Ap
30	40	37.7	174	10	US-09-864-761-38950	Sequence 38950, A
31	40	37.7	339	10	US-09-925-297-704	Sequence 704, App
32	40	37.7	382	9	US-09-738-626-6012	Sequence 6012, App
33	40	37.7	385	10	US-09-925-300-1174	Sequence 1174, Ap
34	40	37.7	948	10	US-09-888-615-94	Sequence 94, Appl
35	40	37.7	1148	10	US-09-815-242-11895	Sequence 11895, A
36	40	37.7	2237	12	US-10-033-026-8	Sequence 8, Appl1
37	40	37.7	2336	12	US-10-033-026-10	Sequence 10, Appl1
38	40	37.7	2339	12	US-10-033-026-6	Sequence 6, Appl1
39	40	37.7	2343	12	US-10-033-026-4	Sequence 4, Appl1
40	39.5	37.3	426	10	US-09-764-864-809	Sequence 809, App
41	39.5	37.3	664	10	US-09-780-525-2	Sequence 2, Appl1
42	39	36.8	41	10	US-09-864-761-36486	Sequence 36486, A
43	39	36.8	73	10	US-09-925-302-543	Sequence 543, App
44	39	36.8	111	10	US-09-764-847-761	Sequence 761, App
45	39	36.8	130	9	US-10-001-857-205	Sequence 205, App

ALIGNMENTS

RESULT 1
US-09-876-204-3
Sequence 3, Application US/09876204
Patent No. US20020052316A1
GENERAL INFORMATION:
APPLICANT: Gordon C. Shore et al.
TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
FILE REFERENCE: 50013/011001
CURRENT APPLICATION NUMBER: US/09/876, 204
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/166, 028
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-876-204-3

Query Match 100.0%; Score 106; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEOPRGCGPTSSSEQIM 20
Db 1 MDGSGEOPRGCGPTSSSEQIM 20

RESULT 2
US-09-033-525-2
Sequence 2, Application US/09033525
Patent No. US20020090374A1
GENERAL INFORMATION:
APPLICANT: Yaikoni, Shai
APPLICANT: Ben-Yehudah, Ahmi
APPLICANT: Azar, Yehudith
APPLICANT: Ageliani, Rami
APPLICANT: Belotitskiy, Ruth
APPLICANT: Lorberbaum-Galski, Haya
TITLE OF INVENTION: CHIMERIC PROTEINS WITH CELL-TARGETING

FT CONFLICT 378 378 ECOR40, ECOR49, ECOR50 ABD ECOR65).

FT SEQUENCE 618 AA; 67233 MW; EBB551C3E2946AC3 CRC64;

Query Match 47.4%; Score 37; DB 1; Length 618;

Best Local Similarity 42.1%; Pred. No. 25; Mismatches 8; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 1 MDGSGXXXXXGPTSSPQI 19
|||
DB 338 MDGEFTOGNVGDTTAQI 356

Job time : 9.30769 secs

RESULT 15

HS73_BOVIN ID HS73_BOVIN STANDARD; PRT; 631 AA.

AC P34933; 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Heat shock 70 kDa protein 3.

GN HSP70-3.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-93122795; PubMed-1478667;

RA Grosz M.D., Momack J.E., Skow L.C.;

RT "Synthetic conservation of HSP70 genes in cattle and humans.";

RL Genomics 14:863-868(1992).

CC -I- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE

CC PREEXISTENT PROTEINS AGAINST AGGREGATION AND MEDiate THE FOLDING

CC OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN

CC ORGANELLES. THESE CHAPERONES PARTICIPATE IN ALL THESE PROCESSES

CC THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE CONFORMATIONS OF

CC OTHER PROTEINS. THEY BIND EXTENDED PEPTIDE SEGMENTS WITH A NET

CC HYDROPHOBIC CHARACTER EXPOSED BY POLYPEPTIDES DURING TRANSLATION

CC AND MEMBRANE TRANSLOCATION, OR FOLLOWING STRESS-INDUCED DAMAGE.

CC -I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL: L10428; AAA30569.1; -

DR HSP; P19120; 3HSC.

DR InterPro: IPR001023; Hsp70.

DR Pfam: PF00012; HSP70; 1.

DR PRINTS: PR00301; HEATSHOCK70.

DR PRODOM: PD000089; HSP70; 1.

DR PROSITE: PS00287; HSP70_1; 1.

DR PROSITE: PS00329; HSP70_2; 1.

DR PROSITE: PS01036; HSP70_3; 1.

KW ATP-binding; Chaperone; Heat shock; Multigene family.

SO SEQUENCE 631 AA; 69199 MW; 01ACA20600C9322F CRC64;

Query Match 47.4%; Score 37; DB 1; Length 631;

Best Local Similarity 46.7%; Pred. No. 26; Mismatches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 GSGGXXXXXGPTSSSE 17
| | | | |
DB 615 GGGGSGAGGPTIEE 629

Search completed: January 7, 2003, 12:29:50

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CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL: X52633; CA36858.1; -.
DR EMBL: Z28264; CA82113.1; -.
DR PIR: S38111; S38111.
DR SGD: S0001747; GAPI.
DR InterPro: IPR002293; AA/rel_pmease1.
DR InterPro: IPR004840; AAC_pernase.
DR InterPro: IPR004841; Pernase.
DR InterPro: IPR004762; Yeast_AA_pern.
DR Pfam: PF00324; aa_pernases; 1.
DR TIGRFAMs: TIGR00913; 2A0310; 1.
DR PROSITE: PS00218; AMINO_ACID_PERMEASE_1; 1.
KM Transport: Amino-acid transport; Transmembrane.
FT TRANSMEM 96 116 POTENTIAL.
FT TRANSMEM 122 142 POTENTIAL.
FT TRANSMEM 166 185 POTENTIAL.
FT TRANSMEM 205 224 POTENTIAL.
FT TRANSMEM 238 256 POTENTIAL.
FT TRANSMEM 281 298 POTENTIAL.
FT TRANSMEM 322 342 POTENTIAL.
FT TRANSMEM 377 396 POTENTIAL.
FT TRANSMEM 422 442 POTENTIAL.
FT TRANSMEM 452 472 POTENTIAL.
FT TRANSMEM 492 510 POTENTIAL.
FT TRANSMEM 530 548 POTENTIAL.
FT TRANSMEM 122 122 MISSING (IN REF. 1).
FT CONFLICT 189 189 S -> A (IN REF. 1).
FT CONFLICT 338 338 I -> V (IN REF. 1).
FT CONFLICT 518 518 V -> L (IN REF. 1).
SQ SEQUENCE 602 AA; 65655 MW; 5363616447907458 CRC64;

Query Match 47.4%; Score 37; DA 1; Length 602;
Best Local Similarity 53.8%; Match No. 24;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 GSGXXXXXXGGPTS 15
Db 111 111 1
111 GSGTALRTGCPAS 123

RESULT 14
SPPA_ECOLI STANDARD: PRT: 618 AA.
AC P08395; P77752; Q46723; Q46724; Q46725; Q46726; Q57183;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protease IV (EC 3.4.21.-) (Endopeptidase IV) (Signal peptide
DE peptidase).
GN SPPI OR B1766.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
ON NCBI_TaxID=562;
RX MEDLINE=9742617; PubMed=9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).

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RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28,040.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [4]
RP SEQUENCE OF 110-433 FROM N.A.
RC STRAIN=Various ECOR strains;
RX MEDLINE=95064015; PubMed=7973728;
RA Gutman D.S., Dykhuizen D.E.;
RT "Clonal divergence in Escherichia coli as a result of recombination,
RT not mutation.";
RL Science 266:1380-1383(1994).
CC -!- FUNCTION: DIGESTION OF THE CLEAVED SIGNAL PEPTIDES. THIS ACTIVITY
CC IS NECESSARY TO MAINTAIN PROPER SECRETION OF MATURE PROTEINS
CC ACROSS THE MEMBRANE.
CC -!- SUBUNIT: HOMOTETRAMER.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S49.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL: M13359; AAA24648.1; -.
DR EMBL: AE000271; AAC74836.1; -.
DR EMBL: D90820; BAA15557.1; -.
DR EMBL: U13772; AAA57008.1; -.
DR EMBL: U13773; AAA57009.1; -.
DR EMBL: U13774; AAA57010.1; -.
DR EMBL: U13775; AAA57011.1; -.
DR EMBL: U13776; AAA57012.1; -.
DR EMBL: U13777; AAA57013.1; -.
DR EMBL: U13778; AAA57014.1; -.
DR EMBL: U13779; AAA57015.1; -.
DR EMBL: U13780; AAA57016.1; -.
DR EMBL: U13782; AAA57017.1; -.
DR EMBL: U13833; AAA57030.1; -.
DR EMBL: U13834; AAA57031.1; -.
DR PIR: A24813; PREC74.
DR MEROPS: S49.001; -.
DR Ecogene: EG10968; SPPI.
DR InterPro: IPR002142; Peptidase_U7.
DR InterPro: IPR004635; SigPase_SPPA67.
DR InterPro: IPR004634; SigPase_SPPA67.
DR Pfam: PF01343; Peptidase_U7; 2.
DR ProDom: PD002897; Peptidase_U7; 1.
DR TIGRFAMs: TIGR00705; SPPI_67K; 1.
DR TIGRFAMs: TIGR00706; SPPI_dom; 1.
KW Hydrolase; Protease; Transmembrane; Inner membrane; Complete proteome.
FT TRANSMEM 29 45 POTENTIAL.
FT TRANSMEM 398 414 POTENTIAL.
FT TRANSMEM 421 441 POTENTIAL.
FT VARIANT 151 151 V -> I (IN STRAINS ECOR49 AND ECOR50).
FT VARIANT 186 186 G -> S (IN STRAIN ECOR16).
FT VARIANT 252 252 E -> H (IN STRAIN ECOR16).
FT VARIANT 252 252 E -> K (IN STRAIN ECOR49).
FT VARIANT 252 252 E -> Q (IN STRAINS ECOR38, ECOR39,
FT ECOR40, ECOR50, ECOR65 AND ECOR68).
FT VARIANT 294 294 A -> T (IN STRAINS ECOR38, ECOR39,

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CC EMBL: D10730; BAA01573.1; -
 CC PIR: S27501; S27501.
 CC HSP: P00782; 1501.
 CC MEROPS: S08.030; -
 CC InterPro: IPR000209; Peptidase_S8.
 CC Pfam: PF00082; Peptidase_S8; 1.
 CC PRINTS: PR00723; SUBTILISIN.
 CC PROSITE: PS00136; SUBTILASE_ASP; 1.
 CC PROSITE: PS00137; SUBTILASE_HIS; 1.
 CC PROSITE: PS00138; SUBTILASE_SER; 1.
 CC Hydrolase: Serine protease.
 CC ACT_SITE 49 49 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC ACT_SITE 86 86 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC ACT_SITE 250 250 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC SEQUENCE 321 AA; 33747 MW; 621168D9F1044026 CRC64;

Query Match 47.4%; Score 37; DB 1; Length 321;
 Best Local Similarity 66.7%; Pred. No. 12;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 11 GGPSSSEQ1 19
 DB 155 GGPTDSEEL 163

RESULT 12
 YH83_SCHPO STANDARD; PRT; 579 AA.
 ID YH83_SCHPO
 AC Q9P5N2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Putative amino-acid permease C359.03c.
 GN SPBC359.03c.
 OS Schizosaccharomyces pombe (Fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsis K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grymoprez B.,
 RA Wellens I., Wolstels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel K., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Punnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garçon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Cerrutis A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Drenth L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
 RA "The genome sequence of Schizosaccharomyces pombe";
 RL Nature 415:871-880(2002).

CC -! SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -! SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
 CC -----
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CC EMBL: AL356012; CAB91572.1; -
 CC InterPro: IPR002293; AA/rel_pmeasel.
 CC InterPro: IPR004840; AAC_permease.
 CC InterPro: IPR004841; Permease.
 CC Pfam: PF00324; aa_permeases; 1.
 CC PROSITE: PS00218; AMINO_ACID_PERMEASE_1; 1.
 CC Hypothetical protein; Transport; Amino-acid transport; Transmembrane.
 CC TRANSMEM 109 129 POTENTIAL.
 CC TRANSMEM 188 208 POTENTIAL.
 CC TRANSMEM 216 236 POTENTIAL.
 CC TRANSMEM 304 324 POTENTIAL.
 CC TRANSMEM 348 368 POTENTIAL.
 CC TRANSMEM 402 422 POTENTIAL.
 CC TRANSMEM 472 492 POTENTIAL.
 CC TRANSMEM 514 534 POTENTIAL.
 CC SEQUENCE 579 AA; 63259 MW; C60DFABE64397CD3 CRC64;

Query Match 47.4%; Score 37; DB 1; Length 579;
 Best Local Similarity 53.8%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 3 GSGXXXXXGGPTS 15
 DB 98 GSGSALADCGPAS 110

RESULT 13
 GAP1_YEAST STANDARD; PRT; 602 AA.
 ID GAP1_YEAST
 AC P19145;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE General amino-acid permease GAP1.
 GN GAP1 OR YKR039W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90306009; PubMed=2194797;
 RA Jauniaux J.-C., Gresson M.;
 RA "GAP1, the general amino acid permease gene of Saccharomyces
 RA cerevisiae. Nucleotide sequence, protein similarity with the other
 RA bakers yeast amino acid permeases, and nitrogen catabolite
 RA repression";
 RL Eur. J. Biochem. 190:39-44(1990).
 RL [2]
 RP SEQUENCE FROM N.A.
 RA Uristarazu L.A., Jauniaux J.-C.;
 RA Submitted (MAR-1994) to the EMBL/Genbank/DBJ databases.
 RL -! FUNCTION: PERMEASE FOR VARIOUS AMINO ACIDS AS WELL AS FOR GABA.
 CC -! SUBCELLULAR LOCATION: Integral membrane protein.
 CC -! SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>


```

RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,
RA Gallibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombe W.R., Paulsen I., Potashkin J.,
RA Shipakovsky G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -1- FUNCTION: PHP2 IS A GLOBAL REGULATOR OF RESPIRATORY FUNCTIONS IN
CC YEAST CELLS. IT BELONGS TO A COMPLEX THAT BINDS TO THE SEQUENCE
CC CCAAT LOCATED UPSTREAM OF GENES INVOLVED IN MITOCHONDRIAL ELECTRON
CC TRANSPORT.
CC -1- SUBUNIT: BELONGS TO AN HETEROTRIMERIC CCAAT-BINDING COMPLEX (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE CBF-B SUBUNIT FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M63639; AAA35322.1; -
DR AL034352; CAA22183.1; -
DR PIR: A39605; A39605.
DR TRANSFAC: T00348; -
DR InterPro: IPR001289; TF_CBF.
DR Pfam: PF02045; CBF_B_NFYA.1.
DR PRINTS: PR00616; CCAATSUBUNT.
DR ProDom: PD003860; TF_CBF.1.
DR SMART: SM00521; CBF_1.
DR PROSITE: PS00686; CBF_B_NFYA.1.
DR DNA-binding; Transcription regulation; Activator; Nuclear protein.
FT DOMAIN 11 743
FT IMPORTANT FOR SUBUNIT INTERACTIONS.
FT (BY SIMILARITY).
FT BY SIMILARITY.
FT DNA_BIND 44 64
FT DOMAIN 224 231
FT SER/THR-RICH.
FT SEQUENCE 334 AA: 34893 MW: 785829BC2CA27B6 CRC64:
SQ
Query Match 48.7%; Score 38; DB 1; Length 334;
Best Local Similarity 43.8%; Pred. No. 8.2;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 MGSGXXXXXGPTSS 16
DB 165 LDMSGNIAMSGPTNT 180

```

```

RT (the xylC gene product) and 2-hydroxymuconic semialdehyde
RT dehydrogenase (the xylG gene product) encoded by TOL plasmid pMW0 of
RT Pseudomonas putida.";
RL J. Bacteriol. 177:1196-1201(1995).
RN [2]
RP SEQUENCE OF 1-53.
RC PLASMID=TOL pMW53;
RX MEDLINE=91113163; PubMed=1989592;
RA Chalmers R.M., Keen J.N., Fawson C.A.;
RT "Comparison of benzyl alcohol dehydrogenases and benzaldehyde
RT dehydrogenases from the benzyl alcohol and mandelate pathways in
RT Acinetobacter calcoaceticus and from the TOL-plasmid-encoded toluene
RT pathway in Pseudomonas putida. N-terminal amino acid sequences, amino
RT acid compositions and immunological cross-reactions.";
RL Biochem. J. 273:99-107(1991).
CC -1- CATALYTIC ACTIVITY: Benzaldehyde + NAD(+) + H(2O) = benzoate +
CC NADH.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- MISCELLANEOUS: OPTIMAL PH FOR ACTIVITY IS 9.0.
CC -1- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U15151; AAA66218.1; -
DR EMBL: D63341; BAA09661.1; -
DR HSSP: P51977; IBXS.
DR InterPro: IPR002086; Aldehyde_dehydr.
DR Pfam: PF00171; aldehyd.1.
DR PROSITE: PS00070; ALDEHYDE_DEHYDR_CYS.1.
DR PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU.1.
DR Aromatic hydrocarbons catabolism; Oxidoreductase; NAD; Plasmid.
FT NP_BIND 232 237
FT ACT SITE 254 254
FT ACT SITE 288 288
FT BY SIMILARITY.
FT BY SIMILARITY.
FT SEQUENCE 487 AA: 51897 MW: 093CB3E9487AF84 CRC64:
SQ
Query Match 48.7%; Score 38; DB 1; Length 487;
Best Local Similarity 44.4%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
QY 1 MGSGXXXXXGPTSSQ 18
DB 452 MGASGSGRPGPASIIE 469

```

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RESULT 10
XYL_C_PSEPU
ID XYL_C_PSEPU STANDARD: PRT; 487 AA.
AC P43503;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Benzaldehyde dehydrogenase [NAD+] (EC 1.2.1.28).
OS XYL_C.
OS Pseudomonas putida.
OC Plasmid TOL pMW0, and Plasmid TOL pMW53.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.
RC PLASMID=TOL pMW0;
RX MEDLINE=95173094; PubMed=7868591;
RA Inoue J., Shaw J.P., Reikik M., Harayama S.;
RT "Overlapping substrate specificities of Benzaldehyde dehydrogenase

```

```

ISP_BACCS
ID ISP_BACCS STANDARD: PRT; 321 AA.
AC P29140;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Intracellular alkaline protease (EC 3.4.21.-).
OS Bacillus clausii.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=79880;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=221 / ATCC 21522 / JCM 9139 / DSM 2512;
RA Kato C., Nakano Y., Yamamoto M., Horikoshi K.;
RL Submitted (MAR-1992) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```



```
; Sequence 161, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L.Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 14
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-161

Query Match          25.0%; Score 5; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DSGGE 6
      |||||
DB      5 DSGGE 9

RESULT 15
US-09-826-290-294
; Sequence 294, Application US/09826290
; Patent No. US20020164668A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L.Kathryn
; APPLICANT: Friedman, David L.
; APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
; APPLICANT: Kimmel, Lida H.
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Potter, David M.
; APPLICANT: Rohlf, Christian
; APPLICANT: Silber, B. Michael
; APPLICANT: Stiger, Thomas R.
; APPLICANT: Sunderland, P. Trey
; APPLICANT: Townsend, Robert Reid
; APPLICANT: White, Frost
; APPLICANT: Williams, Stephen A.
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
; TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
; FILE REFERENCE: 2572-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/826,290
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/194,504
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/253,647
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 492
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 294
; LENGTH: 14
; TYPE: PRT
; ORGANISM: homo sapien
US-09-826-290-294

Query Match          25.0%; Score 5; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DSGGE 6
      |||||
DB      5 DSGGE 9
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Search completed: January 7, 2003, 12:46:23
Job time : 7.69231 secs

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;
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/850,048A
; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/609,187
; FILING DATE: 1996-03-01
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-028-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-850-048A-2

Query Match
Best Local Similarity 100.0%; Score 6; DB 10; Length 730;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RCGGP 13
|||||
DB 191 RCGGP 196

RESULT 11
US-09-978-698-2
; Sequence 2, Application US/09978698
; Patent No. US20020151010A1
; GENERAL INFORMATION:
; APPLICANT: Ravapatti, P. John
; TITLE OF INVENTION: Regulation of Carbon Assimilation
; FILE REFERENCE: 1533.0930001
; CURRENT APPLICATION NUMBER: US/09/978,698
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 09/606,312
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 966
; TYPE: PRT
; ORGANISM: Medicago sativa
US-09-978-698-2

Query Match
Best Local Similarity 30.0%; Score 6; DB 10; Length 966;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RCGGP 14
|||||
```

```

DB 642 RCGGP 647

RESULT 12
US-09-968-561A-156
; Sequence 156, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligand
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 156
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-156

Query Match
Best Local Similarity 25.0%; Score 5; DB 9; Length 9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RCGGP 13
|||||
DB 3 RCGGP 7
```

```

RESULT 13
US-09-192-854-89
; Sequence 89, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-89

Query Match
Best Local Similarity 25.0%; Score 5; DB 10; Length 9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RCGGP 13
|||||
DB 3 RCGGP 7

RESULT 14
US-09-826-290-161
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US-09-925-301-1634

Query Match 30.0%; Score 6; DB 10; Length 88;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PRGSGP 13
|||||
DB 22 PRGSGP 27

RESULT 7

US-09-876-889-16
; Sequence 16, Application US/09876889
; Patent No. US20020076715A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
; FILE REFERENCE: 210121.466C3
; CURRENT APPLICATION NUMBER: US/09/876.889
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-876-889-16

Query Match 30.0%; Score 6; DB 10; Length 154;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 PRSSEQ 18
|||||
DB 64 PRSSEQ 69

RESULT 8

US-10-067-813-17
; Sequence 17, Application US/10067813
; Patent No. US20020156013A1
; GENERAL INFORMATION:
; APPLICANT: Renauld, Jean-Christophe
; APPLICANT: Louahed, Jamila
; APPLICANT: Grassio, Luigi
; APPLICANT: Levilt, Roy
; APPLICANT: Nicolaides, Nicholas
; TITLE OF INVENTION: Asthma Associated Factors as Targets for Treating
; FILE REFERENCE: 036870-5071
; CURRENT APPLICATION NUMBER: US/10/067.813
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/157,247
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 218
; TYPE: PRT
; ORGANISM: R-Ras
US-10-067-813-17

Query Match 30.0%; Score 6; DB 9; Length 218;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PRGSGP 13
|||||

DB 14 PRGSGP 19

RESULT 9

US-10-143-002-4
; Sequence 4, Application US/10143002
; Patent No. US20020132775A1
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Potassium Channel Protein 1
; and 2
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: CARELLA, BYRNE, BAIN, GILFILLAN,
; CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/143,002
; FILING DATE: 13-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,493
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/468,533
; FILING DATE: 6 JUNE 1995
; APPLICATION NUMBER: PCT/US94/08449
; FILING DATE: 28 JUL 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-310
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 494 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS: <Unknown>
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-143-002-4

Query Match 30.0%; Score 6; DB 12; Length 494;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGE 6
|||||
DB 1 MDGSGE 6

RESULT 10
US-09-850-048A-2
; Sequence 2, Application US/09850048A
; Patent No. US20020037574A1
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; hojima, Yoshio
; Li, Shi-Wu
; Sieron, Aleksander
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
; PROCESSES, METHODS AND USES THEREOF

```

: TITLE INVENTION: SPECIFICITY AND APOPTOSIS-INDUCING ACTIVITIES
:
: FILE REFERENCE: 945/-009-999
:
: CURRENT APPLICATION NUMBER: US/09/033,525
:
: CURRENT FILING DATE: 1998-03-02
:
: NUMBER OF SEQ ID NOS: 10
:
: SOFTWARE: FastSeq for Windows Version 3.0
:
: SEQ ID NO 2
:
: LENGTH: 331
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
US-09-033-525-2

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Query Match	95.0%	Score 19:	DB 10:	length 331:
Best Local Similarity	100.0%	Pred. No.	1.7e-11:	
Matches	19:	Conservative	0:	Mismatches 0:
				Indels 0:
				Gaps 0

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QY      2 DSGGEQPRGGGPTSSSEQIM 20
          |||||
Db     141 DSGGEQPRGGGPTSSSEQIM 159
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```

1 RESULT 3
2 US-09-876-204-5
3 : Sequence 5, Application US/09876204
4 : Patent No. US20020052316A1
5 : GENERAL INFORMATION:
6 : APPLICANT: Gordon C. Shore et al.
7 : TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
8 : TITLE OF INVENTION: REAGENTS AND METHODS
9 : FILE REFERENCE: 50013/011001
10 : CURRENT APPLICATION NUMBER: US/09/876,204
11 : CURRENT FILING DATE: 2001-06-06
12 : PRIOR APPLICATION NUMBER: 09/166, 028
13 : PRIOR FILING DATE: 1998-10-05
14 : NUMBER OF SEQ. ID NOS.: 7
15 : SOFTWARE: FastSeq for Windows Version 4.0
16 : SEQ. ID NO 5
17 : LENGTH: 20
18 : TYPE: PRT
19 : ORGANISM: Rattus norvegicus
20 : US-09-876-204-5

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Query Match	55.0%	Score 11:	DB 10:	length 20:
Best Local Similarity	100.0%	Pred. No.	7.3e-05:	
Matches 11, Conservative	0:	Mismatches	0:	Indels 0: Gaps 0

QY	10	GGGPTSSSEQIM	20
Db	10	GGGPTSSSEQIM	20

```

RESULT 4
US-09-876-204-4
: Sequence 4, Application US/09876204
: Patent No. US20020052316A1
: GENERAL INFORMATION:
: APPLICANT: Gordon C. Shore et al.
: TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
: FILE OF INVENTION: REAGENTS AND METHODS
: FILE REFERENCE: 50013/011001
: CURRENT APPLICATION NUMBER: US/09/876,204
: CURRENT FILING DATE: 2001-06-06
: PRIOR APPLICATION NUMBER: 09/166,028
: PRIOR FILING DATE: 1998-10-05
: NUMBER OF SEQ. ID NOS: 7
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO. 4
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Mus musculus
: US-09-876-204-4

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Query Match	50.0%; Score 10; DB 10; Length 20;
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Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 11 GGPtSSEQIM 20
      |||||
Db 11 GGPtSSEQIM 20
```

```

RESULT 5
US-09-876-204-1
Sequence 1, Application US/09876204
Patent No. US20020052316A1
GENERAL INFORMATION:
APPLICANT: Gordon C. Shore et al.
TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
TITLE OF INVENTION: RAGENTS AND METHODS
FILE REFERENCE: 50013/011001
CURRENT APPLICATION NUMBER: US/09/876,204
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/156,028
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic based on consensus sequence of Homo
OTHER INFORMATION: sapiens, Mus musculus, and Rattus norvegicus
NAME/KEY: VARIANT
LOCATION: (6)...(10)
OTHER INFORMATION: Xaa at 6 can be E or D; Xaa at 7 can be Q or H
OTHER INFORMATION: Xaa at 8 can be L or P; Xaa at 9 can be R or G;
OTHER INFORMATION: Xaa at 10 can be S or G;
US-09-876-204-1

```

Query Match	45.0%	Score 9;	DB 10;	Length 19;
Best Local Similarity	100.0%	Pred. No. 0.0057;		
Matches	9;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;

QY	11	GGPTSSEQI	19
Db	11	GGPTSSEQI	19

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1      RESULT 6
2      US-09-925-301-1634
3      Sequence 1634, Application US/09925301
4      Patent No. US20020052308A1
5      GENERAL INFORMATION:
6      APPLICANT: Rosen et al.
7      TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
8      FILE REFERENCE: PA106
9      CURRENT APPLICATION NUMBER: US/09/925,301
10     CURRENT FILING DATE: 2001-08-10
11     PRIOR APPLICATION NUMBER: PCT/US00/05882
12     PRIOR FILING DATE: 2000-03-08
13     PRIOR APPLICATION NUMBER: 60/124,270
14     PRIOR FILING DATE: 1999-03-12
15     NUMBER OF SEQ ID NOS: 1694
16     SOFTWARE: PatentIn Ver. 2.0
17     SEQ ID NO 1634
18     LENGTH: 88
19     TYPE: PRT
20     ORGANISM: Homo sapiens
21     FEATURE:
22     NAME/KEY: SITE
23     LOCATION: (82)
24     OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
25     NAME/KEY: SITE
26     LOCATION: (88)
27     OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:39:54 : Search time 7.69231 Seconds
(without alignments)
49.274 Million cell updates/sec

Title: US-09-876-204-3
Perfect score: 20
Sequence: 1 MDGSGEOPRGGPTSEQIM 20

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 117078 seqs, 18951520 residues

Word size : 0

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/PCITUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	10 US-09-876-204-3	Sequence 3, Appli
2	19	95.0	331	10 US-09-033-525-2	Sequence 2, Appli
3	11	55.0	20	10 US-09-876-204-5	Sequence 5, Appli
4	10	50.0	20	10 US-09-876-204-4	Sequence 4, Appli
5	9	45.0	19	10 US-09-876-204-1	Sequence 1, Appli
6	6	30.0	88	10 US-09-925-301-1634	Sequence 1634, Ap
7	6	30.0	154	10 US-09-876-889-16	Sequence 16, Appl
8	6	30.0	218	9 US-10-067-813-17	Sequence 17, Appl
9	6	30.0	494	12 US-10-143-002-4	Sequence 4, Appli
10	6	30.0	730	10 US-09-850-048A-2	Sequence 2, Appli
11	6	30.0	966	10 US-09-978-698-2	Sequence 2, Appli
12	5	25.0	9	9 US-09-968-561A-156	Sequence 156, App
13	5	25.0	14	9 US-09-192-854-89	Sequence 89, Appl
14	5	25.0	14	9 US-09-826-290-161	Sequence 161, App
15	5	25.0	14	9 US-09-826-290-284	Sequence 294, App
16	5	25.0	14	9 US-09-826-290-304	Sequence 304, App
17	5	25.0	14	9 US-09-791-378-92	Sequence 92, Appl
18	5	25.0	14	10 US-09-791-378-142	Sequence 142, App
19	5	25.0	14	10 US-09-791-378-154	Sequence 154, App

20	5	25.0	14	10 US-09-791-378-266	Sequence 266, App
21	5	25.0	14	10 US-09-791-378-383	Sequence 383, App
22	5	25.0	14	10 US-09-791-378-385	Sequence 385, App
23	5	25.0	14	10 US-09-791-378-438	Sequence 438, App
24	5	25.0	14	10 US-09-791-378-532	Sequence 532, App
25	5	25.0	14	10 US-09-791-378-534	Sequence 534, App
26	5	25.0	16	10 US-09-916-940-85	Sequence 85, Appl
27	5	25.0	16	10 US-09-916-940-97	Sequence 97, Appl
28	5	25.0	16	10 US-09-918-063-9	Sequence 9, Appl1
29	5	25.0	32	10 US-09-918-063-33	Sequence 33, Appl
30	5	25.0	37	10 US-09-205-658-357	Sequence 257, App
31	5	25.0	38	10 US-09-864-761-41953	Sequence 41953, A
32	5	25.0	46	10 US-09-864-761-44901	Sequence 34901, A
33	5	25.0	46	10 US-09-864-761-48989	Sequence 48989, A
34	5	25.0	48	10 US-09-918-063-9	Sequence 9, Appl1
35	5	25.0	49	10 US-09-864-761-35963	Sequence 35963, A
36	5	25.0	50	10 US-09-864-761-38835	Sequence 38835, A
37	5	25.0	51	10 US-09-864-761-48301	Sequence 48301, A
38	5	25.0	51	10 US-09-918-063-24	Sequence 24, Appl
39	5	25.0	64	10 US-09-864-761-33529	Sequence 33529, A
40	5	25.0	67	10 US-09-867-550-456	Sequence 456, App
41	5	25.0	71	8 US-08-424-550B-309	Sequence 309, App
42	5	25.0	71	9 US-09-764-884-28	Sequence 28, Appl
43	5	25.0	73	10 US-09-925-302-543	Sequence 543, App
44	5	25.0	76	10 US-09-864-761-36343	Sequence 36343, A
45	5	25.0	77	9 US-10-001-835-143	Sequence 143, App

ALIGNMENTS

RESULT 1
US-09-876-204-3
Sequence 3, Application US/09876204
Patent No. US20020052316A1
GENERAL INFORMATION:
APPLICANT: Gordon C. Shore et al.
TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
FILE REFERENCE: 50013/011001
CURRENT APPLICATION NUMBER: US/09/876,204
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/166,028
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-876-204-3

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1,8e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEOPRGGPTSEQIM 20
DB 1 MDGSGEOPRGGPTSEQIM 20

RESULT 2
US-09-033-525-2
Sequence 2, Application US/09033525
Patent No. US20020090374A1
GENERAL INFORMATION:
APPLICANT: Yarkoni, Shai
APPLICANT: Ben-Yehudai, Ahmi
APPLICANT: Azar, Yehudith
APPLICANT: Agellian, Rami
APPLICANT: Belotskiy, Ruth
APPLICANT: Lorberbaum-Galski, Haya
TITLE OF INVENTION: CHIMERIC PROTEINS WITH CELL-TARGETING

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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:37:03 ; Search time 13.3333 Seconds
(without alignments)
144.202 Million cell updates/sec

Title: US-09-876-204-3

Perfect score: 20
Sequence: 1 MDGSGEOPRCGGPTSSSQIM 20

Scoring table: OLIGO
Gapop 60.0 , Capext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR_73:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	143	2 I38921	bcl-2-associated p
2	20	100.0	179	2 JC7255	Bax-delta protein
3	20	100.0	192	2 A47538	bcl-2-associated p
4	20	100.0	218	2 B47538	bcl-2-associated p
5	11	55.0	41	2 C47538	bcl-2-associated p
6	10	50.0	192	2 D47538	bcl-2-associated p
7	9	45.0	743	2 T47849	hypothetical prote
8	8	40.0	531	2 T08760	hypothetical prote
9	7	35.0	968	2 T51933	kinesin motor prot
10	7	35.0	1217	2 T00270	hypothetical prote
11	6	30.0	105	2 PM0018	hypothetical prote
12	6	30.0	126	2 T16952	hypothetical prote
13	6	30.0	137	2 G72666	hypothetical prote
14	6	30.0	218	1 TVH0R	transforming prote
15	6	30.0	246	2 B37225	acrosomal protein
16	6	30.0	265	2 A37225	interphotoreceptor
17	6	30.0	297	2 S33927	interphotoreceptor
18	6	30.0	298	2 S27965	hypothetical prote
19	6	30.0	302	2 S71334	acetyl xylan ester
20	6	30.0	304	2 A49185	interphotoreceptor
21	6	30.0	311	2 T15997	hypothetical prote
22	6	30.0	337	2 I47079	follicularin - shes
23	6	30.0	344	1 A27701	follicularin - precu
24	6	30.0	344	2 T45894	follicularin - bovi
25	6	30.0	348	2 T26528	hypothetical prote
26	6	30.0	364	2 I45915	interstitial retin
27	6	30.0	370	2 S68415	phosphoenolpyruvat
28	6	30.0	370	2 S68416	phosphoenolpyruvat
29	6	30.0	371	2 S68413	phosphoenolpyruvat

30	6	30.0	371	2 S68414	phosphoenolpyruvat
31	6	30.0	382	2 T29681	hypothetical prote
32	6	30.0	397	2 H72668	hypothetical prote
33	6	30.0	411	2 PC2168	phosphoenolpyruvat
34	6	30.0	411	2 E96665	protein F22C12.16
35	6	30.0	416	2 S72781	probable phosphog
36	6	30.0	431	2 A72549	probable pyruvate
37	6	30.0	441	2 S14441	retinol-binding pr
38	6	30.0	441	2 F48327	COI Intron 5 prote
39	6	30.0	446	2 T09960	mitosis-specific c
40	6	30.0	447	2 T19078	hypothetical prote
41	6	30.0	453	2 PC2167	phosphoenolpyruvat
42	6	30.0	486	2 PC2169	phosphoenolpyruvat
43	6	30.0	494	2 JC5919	potassium channel
44	6	30.0	495	2 T52515	related to n-alkan
45	6	30.0	495	2 A83866	glutamate synthase

ALIGNMENTS

RESULT 1
I38921
bcl-2-associated protein x, delta splice form - human
N:Alternate names: BAX: programmed cell death membrane protein x delta
C:Species: Homo sapiens (man)
C>Date: 09-Mar-1996 #sequence-revision 09-Mar-1996 #text-change 17-Nov-2000
C:Accession: I38921
R:Apte, S.S.; Mattei, M.G.; Olsen, B.R.
Genomics 26, 592-594, 1995
A>Title: Mapping of the human BAX gene to chromosome 19q13.3-q13.4 and isolation of a
A:Reference number: I38921; MID:95311797; PMID:760765
A:Accession: I38921
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-143 <RES>
A:Cross-references: EMBL:U19599; NID:g841237; PIDN:AMC50142.1; PID:g841238
C:Genetics:
A:Gene: GDB:BAX
A:Cross-references: GDB:228082; OMIM:600040
A:Map position: 19q13.3-19q13.4
C:Superfamily: bcl transforming protein

Query Match Best Local Similarity 100.0%; Pred. No. 1e-13; Length 143;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRCGGPTSSSQIM 20
Db 1 MDGSGEOPRCGGPTSSSQIM 20

RESULT 2
JC7255
Bax-delta protein - human
C:Species: Homo sapiens (man)
C>Date: 09-Jun-2000 #sequence-revision 09-Jun-2000 #text-change 17-Nov-2000
C:Accession: JC7255
R:Schmitt, E.; Paquet, C.; Beauchemin, M.; Dever-Bertrand, J.; Bertrand, R.
Biochem. Biophys. Res. Commun. 270, 868-879, 2000
A>Title: Characterization of Bax-delta, a cell death-inducing isoform of Bax.
A:Reference number: JC7255
A:Accession: JC7255
A:Molecule type: mRNA
A:Residues: 1-179 <SCH>
A:Cross-references: GB:AF247393
C:Experimental source: cancer promyelocytic cells
C:Comment: This protein, a member of the Bcl-2 family, has a proapoptotic effect. It
cultivation.
C:Superfamily: bcl transforming protein
C:Keywords: transmembrane protein

Query Match 100.0%; Score 20; DB 2; Length 179;

Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDGSEOPRGCGPTSSSEQIM 20
|||||
Db 1 MDGSEOPRGCGPTSSSEQIM 20

RESULT 3

A47538
bcl1-2-associated protein x, alpha splice form - human
N:Alternate names: BAX; programmed cell death membrane protein x alpha
C:Species: Homo sapiens (man)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C:Accession: A47538
R:Oliva, Z.N.; Millman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates F
A:Reference number: A47538; MUID:93364978; PMID:8358790
A:Accession: A47538
A:Molecule type: mRNA
A:Residues: 1-192 <OLT>
A:Cross-references: GB:L22473; NID:g388165; PIDN:AAA03619.1; PID:g388166
A>Note: the amino end of the mature protein is blocked
C:Genetics:
A:Gene: GDB:BAX
A:Cross-references: GDB:228082; OMIM:600040
A:Map position: 19q13.3-19q13.4
C:Superfamily: bcl transforming protein
C:Keywords: alternative splicing; blocked amino end; heterodimer; homodimer; transmembrane F;172-191/domain; transmembrane #status predicted <TM1>

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 192;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSEOPRGCGPTSSSEQIM 20
|||||
Db 1 MDGSEOPRGCGPTSSSEQIM 20

RESULT 4

B47538
bcl-2-associated protein x, beta splice form - human
N:Alternate names: BAX; programmed cell death membrane protein x beta
C:Species: Homo sapiens (man)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C:Accession: B47538
R:Oliva, Z.N.; Millman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates F
A:Reference number: A47538; MUID:93364978; PMID:8358790
A:Accession: B47538
A:Molecule type: mRNA
A:Residues: 1-218 <OLT>
A:Cross-references: GB:L22474; NID:g388167; PIDN:AAA03620.1; PID:g388168
A>Note: the amino end of the mature protein is blocked
C:Genetics:
A:Gene: GDB:BAX
A:Cross-references: GDB:228082; OMIM:600040
A:Map position: 19q13.3-19q13.4
C:Superfamily: bcl transforming protein
C:Keywords: alternative splicing; blocked amino end; cytosol; heterodimer; homodimer

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 218;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSEOPRGCGPTSSSEQIM 20
|||||
Db 1 MDGSEOPRGCGPTSSSEQIM 20

RESULT 5
C47538
bcl1-2-associated protein x, gamma splice form - human
N:Alternate names: BAX; programmed cell death membrane protein x gamma
C:Species: Homo sapiens (man)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-Oct-1999
C:Accession: C47538
R:Oliva, Z.N.; Millman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerate

A:Reference number: A47538; MUID:93364978; PMID:8358790
A:Accession: C47538
A:Molecule type: mRNA
A:Residues: 1-41 <OLT>
A:Cross-references: GB:L22475; NID:g388169; PIDN:AAA03621.1; PID:g388170
A>Note: the amino end of the mature protein is blocked
C:Genetics:
A:Gene: GDB:BAX
A:Cross-references: GDB:228082; OMIM:600040
A:Map position: 19q13.3-19q13.4
C:Keywords: alternative splicing; blocked amino end; cytosol; heterodimer; homodimer

Query Match
Best Local Similarity 100.0%; Score 11; DB 2; Length 41;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSEOPRGCG 11
|||||
Db 1 MDGSEOPRGCG 11

RESULT 6

D47538
bcl-2-associated protein x - mouse
N:Alternate names: BAX; programmed cell death membrane protein x
C:Species: Mus musculus (house mouse)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C:Accession: D47538
R:Oliva, Z.N.; Millman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerate
A:Reference number: A47538; MUID:93364978; PMID:8358790
A:Accession: D47538
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-192 <OLT>
A:Cross-references: GB:L22472
C:Genetics:
A:Gene: bax
C:Superfamily: bcl transforming protein

Query Match
Best Local Similarity 100.0%; Score 10; DB 2; Length 192;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GGPTSSSEQIM 20
|||||
Db 11 GGPTSSSEQIM 20

RESULT 7

T47849
hypothetical protein T8B10.40 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T47849
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Maye
submitted to the Protein Sequence Database, March 2000
A:Reference number: 224478
A:Accession: T47849
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-743 <RIE>

A:Cross-references: EMBL:AL138646
A:Experimental source: cultivar Columbia; BAC clone T8B10
C:Genetics:
A:Map position: 3
A:Note: T8B10.40

Query Match 45.0%; Score 9; DB 2; Length 743;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SGEQPRGG 12
|||||
DB 725 SGEQPRGG 733

RESULT 8
T08760
hypothetical protein DKFZP586M1019.1 - human
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C:Accession: T08760
R:Manduit, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A:Reference number: 216471
A:Accession: T08760
A:Molecule type: mRNA
A:Residues: 1-531 <MAN>
A:Cross-references: EMBL:AL050284
A:Experimental source: adult uterus; clone DKFZP586M1019
C:Genetics:
A:Note: DKFZP586M1019.1

Query Match 40.0%; Score 8; DB 2; Length 531;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 GEQPRGG 12
|||||
DB 117 GEQPRGG 124

RESULT 9
T51933
kinesin motor protein [imported] - smut fungus (Ustilago maydis)
C:Species: Ustilago maydis (corn smut)
C:Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 31-Dec-2000
C:Accession: T51933
R:Lehmiller, C.; Steinberg, G.; Snetelaar, K.M.; Schliwa, M.; Kahmann, R.; Bolker, M.
EMBO J. 16, 3464-3473, 1997
A:Title: Identification of a motor protein required for filamentous growth in Ustilago m
A:Reference number: 220770; MUID:97361828; PMID:9218789
A:Accession: T51933
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-968 <LEH>
A:Cross-references: EMBL:U92845; PIDN:AAB63337.1
C:Genetics:
A:Gene: Kin2
C:Superfamily: kinesin heavy chain; kinesin motor domain homology

Query Match 35.0%; Score 7; DB 2; Length 968;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 RCGGPTS 15
|||||
DB 921 RCGGPTS 927

RESULT 10
T00270
hypothetical protein KIAA0596 - human (fragment)
C:Species: Homo sapiens (man)

C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C:Accession: T00270
R:Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara,
DNA Res. 5, 31-39, 1998
A:Title: Prediction of the coding sequences of unidentified human genes. IX. The comp
A:Reference number: 214086; MUID:98290545; PMID:9628581
A:Accession: T00270
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1217 <NAG>
A:Cross-references: EMBL:AB011168; NID:g3043715; PIDN:BAA25522.1; PID:g3043716
A:Experimental source: brain
C:Genetics:
A:Note: KIAA0596

Query Match 35.0%; Score 7; DB 2; Length 1217;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SGEQPRG 10
|||||
DB 838 SGEQPRG 844

RESULT 11
PM0018
hypothetical protein 105 - Micromonospora sp. (fragment)
C:Species: Micromonospora sp.
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Oct-1994
C:Accession: PM0018
R:Kelemen, G.H.; Gundliffe, E.; Financek, I.
Gene 98, 53-60, 1991
A:Title: Cloning and characterization of gentamicin-resistance genes from Micromosp
A:Reference number: JG0017; MUID:91192615; PMID:2013410
A:Accession: PM0018
A:Molecule type: DNA
A:Residues: 1-105 <KEK>
A:Cross-references: GB:M55521
A:Note: the authors translated the codon CCG for residues 27, 30, 31, and 37 as Phe a

Query Match 30.0%; Score 6; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GCPTSS 16
|||||
DB 81 GCPTSS 86

RESULT 12
T16952
hypothetical protein T28D9.10 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16952
R:Fulton, L.
submitted to the EMBL Data Library, June 1995
A:Description: The sequence of C. elegans cosmid T28D9.
A:Reference number: 218614
A:Accession: T16952
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-126 <FUL>
A:Cross-references: EMBL:U28738; NID:g861262; PID:g861268; PIDN:AAA6313.1; CESP:T28D
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:T28D9.10
A:introns: 27/1; 62/1; 96/1

Query Match 30.0%; Score 6; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PRGCGP 13
 |||||
 Db 119 PRGCGP 124

RESULT 13

G72666
 hypothetical protein APE0758 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
 C:Accession: G72666
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
 A:Reference number: A72450; MUID:9310339; PMID:10382966
 A:Accession: G72666
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-137 <RAW>
 A:Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79735.1; PID:d1043521; PID:g5104188
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE0758
 C:Superfamily: Aeropyrum pernix hypothetical protein APE0758

Query Match

Best Local Similarity 30.0%; Score 6; DB 2; Length 137;
 Pred. No. 30;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 QPRGGG 12
 |||||
 Db 85 QPRGGG 90

RESULT 14

TVH0R
 transforming protein R-ras - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 19-Jan-2001
 C:Accession: A26159
 R:Low, D.G.; Capon, D.J.; Delwart, E.; Sakaguchi, A.Y.; Naylor, S.L.; Goeddel, D.V. Cell 46, 137-146, 1987
 A:Title: Structure of the human and murine R-ras genes, novel genes closely related to R-ras
 A:Reference number: A26159; MUID:87078390; PMID:3098437
 A:Accession: A26159
 A:Molecule type: DNA
 A:Residues: 1-218 <LOW>
 A:Cross-references: GB:M14949; NID:g190934; PIDN:AAA60256.1; PID:g190936
 C:Genetics:
 A:Gene: GDB:RRAS
 A:Cross-references: GDB:120356; OMIM:165090
 A:Map position: 19q13.3-19qter
 A:introns: 51/3; 81/1; 115/2; 151/3; 191/2
 C:Superfamily: ras transforming protein; translation elongation factor Tu homology
 C:Keywords: GTP binding; lipoprotein; membrane protein; methylated carboxyl end; nucleot F:30-145/Domain: translation elongation factor Tu homology <ETU>
 F:36-43/Region: nucleotide-binding motif A (P-loop)
 F:142-145/Region: GTP-binding NKXD motif
 F:172-174/Region: GTP-binding SAK/L motif
 F:42,43,61,142,143,145,172/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #sta F:215/Binding site: geranyl-geranyl (Cys) (covalent) #status predicted
 F:215/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status predicted

Query Match

Best Local Similarity 30.0%; Score 6; DB 1; Length 218;
 Pred. No. 45;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 PRGCGP 13
 |||||
 Db 14 PRGCGP 19

RESULT 15

B37225
 acrosomal protein SP-10-10 precursor, testicular - human
 C:Species: Homo sapiens (man)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
 C:Accession: B37225
 R:Wright, R.M.; John, E.; Klotz, K.; Flickinger, C.J.; Herr, J.C. Biol. Reprod. 42, 693-701, 1990
 A:Title: Cloning and sequencing of cDNAs coding for the human intra-acrosomal antigen
 A:Reference number: A37225; MUID:90268085; PMID:1693291
 A:Accession: B37225
 A:Molecule type: mRNA
 A:Residues: 1-246 <WRI>
 A:Cross-references: GB:M82967; NID:g338291; PIDN:AAA36625.1; PID:g338292
 A:Experimental source: testis
 A>Note: the authors translated the codon TCC for residue 29 as Phe and CCA for residue C:Keywords: alternative splicing

Query Match

Best Local Similarity 30.0%; Score 6; DB 2; Length 246;
 Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GSGEOP 8
 |||||
 Db 149 GSGEOP 154

Search completed: January 7, 2003, 12:40:23
 Job time: 14.3333 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2003, 12:27:38 : Search time 25.1282 Seconds
(without alignments)
163.997 Million cell updates/sec

Title: US-09-876-204-3

Perfect score: 106
Sequence: 1 MDGSGEOPRGCGPTSSQIM 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_oranelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	100.0	24	08WXU1	08WXU1 homo sapien
2	106	100.0	164	09UQD6	09UQD6 homo sapien
3	106	100.0	179	09NYG7	09NYG7 homo sapien
4	97	91.5	192	08S043	08S043 felis silve
5	83	78.3	24	11 08VHY7	08VHY7 mus musculu
6	54	50.9	302	3 09G034	09G034 trichoderma
7	52	49.1	402	4 09NS06	09NS06 homo sapien
8	52	49.1	403	4 09C009	09C009 homo sapien
9	52	49.1	475	16 092RZ5	092RZ5 rhizobium m
10	51	48.1	658	5 09NR6	09NR6 trypanosoma
11	50	47.2	213	10 09SBR7	09SBR7 medicago va
12	50	47.2	495	12 0918P0	0918P0 ovine herpe
13	50	47.2	743	10 09M221	09M221 arabidopsis
14	49.5	46.7	473	4 09GAV4	09GAV4 homo sapien
15	49.5	46.7	715	4 096JL4	096JL4 homo sapien
16	49.5	46.7	778	4 08TDC2	08TDC2 homo sapien

17	49.5	46.7	794	4 08TDC3	08TDC3 homo sapien
18	49	46.2	310	4 09NX73	09NX73 homo sapien
19	49	46.2	513	16 08U817	08U817 agrobacteri
20	49	46.2	524	4 08WV66	08WV66 homo sapien
21	49	46.2	748	10 08W2R7	08W2R7 oryza sativ
22	49	46.2	1191	5 018414	018414 drosophila
23	48	45.3	137	17 09YE12	09YE12 aeropyrum p
24	47.5	44.8	531	4 09Y3X0	09Y3X0 homo sapien
25	47	44.3	168	11 09DAM3	09DAM3 mus musculu
26	47	44.3	217	4 043770	043770 homo sapien
27	47	44.3	217	4 08W0Z0	08W0Z0 homo sapien
28	47	44.3	217	11 008664	008664 mus musculu
29	46.5	43.9	453	16 08RSN2	08RSN2 streptomyce
30	46.5	43.9	1518	5 09VN58	09VN58 drosophila
31	46	43.4	80	12 064819	064819 human adeno
32	46	43.4	110	12 084879	084879 human adeno
33	46	43.4	404	11 08VD73	08VD73 mus musculu
34	46	43.4	430	5 095RR2	095RR2 drosophila
35	46	43.4	438	5 08WSL0	08WSL0 plasmodium
36	46	43.4	480	5 09VC90	09VC90 drosophila
37	46	43.4	482	12 064837	064837 human adeno
38	46	43.4	523	3 074128	074128 yarrowia 11
39	46	43.4	524	17 027639	027639 methanobact
40	46	43.4	604	15 080880	080880 human immun
41	46	43.4	627	5 062020	062020 caenorhabdi
42	45	42.5	62	16 08YK57	08YK57 mycobacteri
43	45	42.5	92	10 09SNK6	09SNK6 oryza sativ
44	45	42.5	246	13 09PUJ3	09PUJ3 gallus galli
45	45	42.5	331	11 09CWM03	09CWM03 mus musculu

ALIGNMENTS

RESULT 1					
Q8WXU1		PRELIMINARY:	PRT:	24 AA.	
AC 08WXU1:					
DT 01-MAR-2002 (TREMBLrel. 20, Created)					
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)					
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)					
DE BCL2-associated X protein (Fragment).					
GN BAX.					
OS Homo sapiens (Human).					
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
OX NCBI_TaxID=9606;					
RN [1]					
RP SEQUENCE FROM N.A.					
RA Thorndorow E.C., Schwartzfarb E.M., Manfredi J.J.;					
RT "A conserved intronic response element mediates direct p53-dependent					
RT transcriptional activation of both the human and murine bax genes.";					
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.					
DR EMBL; AF339054; AAL73333.1; -					
FT NON TER					
FT 24					
SO SEQUENCE	24 AA;	2379 MW;	8C3D3E8B7479B798	CRC64;	
Query Match					
Best Local Similarity	100.0%;	Score 106;	DB 4;	Length 24;	
Matches 20;	Conservative	0;	Mismatches	0;	
Indels	0;	Caps	0;		
OY 1 MDGSGEOPRGCGPTSSQIM 20					
DB 1 MDGSGEOPRGCGPTSSQIM 20					
RESULT 2					
Q9UQD6		PRELIMINARY:	PRT:	164 AA.	
ID 09UQD6:					
AC 09UQD6:					
DT 01-MAY-2000 (TREMBLrel. 13, Created)					
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)					

DE Bax epsilon.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN.
 RX MEDLINE=9120940; PubMed=9920818;
 RA Shi B., Triebel D., Kajiji S., Iwata K.K., Bruskin A., Mahajna J.,
 RT "Identification and characterization of baxepsilon, a novel bax
 RL Biochem. Biophys. Res. Commun. 254:779-785(1999).
 DR EMBL: AF007826; AAD22706.1; -;
 DR InterPro: IPR000712; Bcl2_BH.
 DR InterPro: IPR002475; Bcl2_family.
 DR Pfam: PF00452; Bcl-2; 1.
 DR SMART: SM00337; BCL; 1.
 DR PROSITE: PSS0062; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01259; BH3; 1.
 SQ SEQUENCE 164 AA; 18129 MW; 12CDB8073EF4C9E CRC64;

Query Match 100.0%; Score 106; DB 4; Length 164;
 Best Local Similarity 100.0%; Pred. No. 5.9e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDGSGEQPRGGGPTSSSEQIM 20
 Db 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 3
 O9ANG7 PRELIMINARY; PRT; 179 AA.
 AC O9ANG7;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Bax-sigma.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20237095; PubMed=10772918;
 RA Schmitt E., Paquet C., Beauchemin M., Dever-Bertrand J., Bertrand R.,
 RT "Characterization of Bax-sigma, a cell death-inducing isoform of
 RT Bax".
 RL Biochem. Biophys. Res. Commun. 270:868-879(2000).
 DR EMBL: AF247393; AAF71267.1; -;
 DR HSSP: Q07817; IMA2.
 DR InterPro: IPR000712; Bcl2_BH.
 DR InterPro: IPR002475; Bcl2_family.
 DR Pfam: PF00452; Bcl-2; 1.
 DR SMART: SM00337; BCL; 1.
 DR PROSITE: PSS0062; BCL2_FAMILY; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01259; BH3; 1.
 SQ SEQUENCE 179 AA; 19718 MW; 5802B0AC73B2E4CE CRC64;

Query Match 100.0%; Score 106; DB 4; Length 179;
 Best Local Similarity 100.0%; Pred. No. 6.5e-09;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MDGSGEQPRGGGPTSSSEQIM 20
 Db 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 4
 O8SQ43

ID O8SQ43 PRELIMINARY; PRT; 192 AA.
 AC O8SQ43;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Bax-protein.
 GN BAX.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamazaki J., Oguma K., Kano R., Hasegawa A.;
 RT "Molecular cloning of feline bcl-2 family";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB080724; BAB5810.1; -;
 SQ SEQUENCE 192 AA; 21283 MW; 852D2771AE86923FB CRC64;

Query Match 91.5%; Score 97; DB 6; Length 192;
 Best Local Similarity 95.0%; Pred. No. 1.8e-07;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MDGSGEQPRGGGPTSSSEQIM 20
 Db 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 5
 O8VHY7 PRELIMINARY; PRT; 24 AA.
 AC O8VHY7;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Bcl2-associated X protein (Fragment).
 GN BAX.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA1B/C;
 RA Thornborough E.C., Schwartzfarb E.M., Manfredi J.J.;
 RT "A conserved intronic response element mediates direct p53-dependent
 RT transcriptional activation of both the human and murine bax genes";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF339055; AAL7334.1; -;
 DR NON_TER 24
 PT 24
 SQ SEQUENCE 24 AA; 2326 MW; 998C7E8B7479A6CC CRC64;

Query Match 78.3%; Score 83; DB 11; Length 24;
 Best Local Similarity 85.0%; Pred. No. 2.9e-06;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MDGSGEQPRGGGPTSSSEQIM 20
 Db 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 6
 O99034 PRELIMINARY; PRT; 302 AA.
 AC O99034;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE ACETYLXYLAN esterase precursor (EC 3.1.1.72).
 GN AXEL.
 OS Trichoderma reesei (Hypocrea jeorina).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; Hypocreaaceae; Hypocrea.

```

OX NCBI_TaxID=51453:
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 158-186, AND CHARACTERIZATION.
RC STRAIN-RUTC-30;
RX MEDLINE=96235218; PubMed=8647098;
RA Margolles-Clark E., Tenkanen M., Soederlund H., Penttilae M.;
RT "Acetyl xylan esterase from Trichoderma reesei contains an active-site
  serine residue and a cellulose-binding domain.";
RL Eur. J. Biochem. 237:553-560(1996).
RN [2]
RP FUNCTION.
RC STRAIN-RUTC-30;
RA Poutanen K., Sundberg M., Korte H., Puls J.;
RT "Deacetylation of xyans by acetyl esterases of Trichoderma reesei.";
RL Appl. Microbiol. Biotechnol. 33:506-510(1990).
RN [3]
RP CHARACTERIZATION.
RC STRAIN-RUTC-30;
RA Sundberg M., Poutanen K.;
RT "Purification and properties of two acetylxylian esterases of
  Trichoderma reesei.";
RL Biotechnol. Appl. Biochem. 13:1-11(1991).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=98437545; PubMed=9761918;
RA Hakulinen N., Tenkanen M., Rouvinen J.;
RT "Crystallization and preliminary X-ray diffraction studies of the
  catalytic core of acetyl xylan esterase from Trichoderma reesei.";
  Acta Crystallogr. D 54:430-432(1998).
CC -1- FUNCTION: DEGRADES ACETYLATED XYLIANS BY CLEAVING ACETYL SIDE
  GROUPS FROM THE HETERO-XYLAN BACKBONE.
CC -1- CATALYTIC ACTIVITY: DEACETYLATION OF XYLIANS AND XYLO-
  OLIGOSACCHARIDES.
CC -1- ENZYME REGULATION: INHIBITED BY PHENYLMETHYLSULFONYL FLUORIDE.
CC -1- PATHWAY: XYLAN DEGRADATION.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- PTM: GLYCOSYLATED.
CC -1- MASS SPECTROMETRY: MW=21806; METHOD=MALDI.
CC -1- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
DR EMBL: Z69236; CA93247.1; -.
DR HSSP: P00725; 2CBH.
DR InterPro: IPR000254; CBD_fungal.
DR InterPro: IPR000675; Cutinase.
DR InterPro: IPR000734; Lipase.
DR Pfam: PF00734; CBM_1; 1.
DR Pfam: PF01083; Cutinase; 1.
DR ProDom: PD001821; CBD_fungal; 1.
DR SMART: SM00236; fCBD; 1.
DR PROSITE: PS00562; CBD_FUNGAL; FALSE NEG.
DR PROSITE: PS00120; LIPASE_SER; UNKNOWN_1.
KM Cellulose degradation; Hydrolyase; Serine esterase; Glycoprotein;
  3D-structure; Signal.
RN [5]
RP SIGNAL
FT SIGNAL 1 20
FT PROPEP 21 31 POTENTIAL.
FT CHAIN 32 302 POTENTIAL.
FT DOMAIN 244 266 ACETYLYLIAN ESTERASE.
FT DOMAIN 267 302 LINKER (BY SIMILARITY).
FT MOD_RES 32 32 CELLULOSE-BINDING (BY SIMILARITY).
FT ACT_SITE 121 121 BLOCKED.
FT ACT_SITE 121 121 BY SIMILARITY.
FT DISULFID 274 291 BY SIMILARITY.
FT DISULFID 285 301 BY SIMILARITY.
FT CAROHID 94 94 N-LINKED (GLCNAC... ) (PROBABLE).
SQ SEQUENCE 302 AA: 30754 MW; B86EDCA2971A9F2A CRC64;

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RESULT 7
ID Q9NS06 PRELIMINARY; PRT; 402 AA.
AC Q9NS06;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Winged helix/forkhead transcription factor.
GN Hfh1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21207067; PubMed=11309849;
RA Hong H.-K., Noveroske J.K., Heaton D.J., Liu T., Sy M.S.,
  Justice M.J., Chakravarti A.;
RT "The winged helix/forkhead transcription factor Foxq1 regulates
  differentiation of hair in satin mice.";
  Genesis 29:163-171(2001).
DR EMBL: AF153341; AAF75586.1; -.
DR HSSP: O63245; 2HFH.
DR InterPro: IPR001766; TF_Fork_head.
DR Pfam: PF00250; Fork_head; 1.
DR PRINTS: PR00053; FORKHEAD.
DR ProDom: PD000425; TF_Fork_head; 1.
DR SMART: SM00339; FH; 1.
DR PROSITE: PS00657; FORK_HEAD_1; 1.
DR PROSITE: PS00658; FORK_HEAD_2; 1.
DR PROSITE: PS50039; FORK_HEAD_3; 1.
SQ SEQUENCE 402 AA: 41485 MW; FD2EEF9DB848E77 CRC64;

Query Match 49.1%; Score 52; DB 4; Length 402;
Best Local Similarity 58.8%; Pred. No. 4.9;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

ID Q9C009 PRELIMINARY; PRT; 403 AA.
AC Q9C009;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE HNF-3/forkhead-like protein 1.
GN Hfh1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bieller A., Pasche B., Frank S., Kunz J., Zoll B.;
RT "Isolation and characterization the human fork head gene Hfh-1.";
  Submitted (JAN-2000) to the EMBL/GenBank/DDb databases.
DR EMBL: AF225950; AKK00639.1; -.
DR HSSP: O63245; 2HFH.
DR InterPro: IPR001766; TF_Fork_head.
DR Pfam: PF00250; Fork_head; 1.
DR PRINTS: PR00053; FORKHEAD.
DR ProDom: PD000425; TF_Fork_head; 1.
DR SMART: SM00339; FH; 1.
DR PROSITE: PS00657; FORK_HEAD_1; 1.
DR PROSITE: PS00658; FORK_HEAD_2; 1.
DR PROSITE: PS50039; FORK_HEAD_3; 1.
SQ SEQUENCE 403 AA: 41491 MW; EB52255AEC6929B CRC64;

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Query Match 49.1%; Score 52; DB 4; Length 403;
Best Local Similarity 58.8%; Pred. No. 4.9;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 GSGEQPRGGGPTSSQI 19
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DB 62 GDGEGSAGGCGAEEAI 78

RESULT 9

Q92R25 PRELIMINARY; PRT; 475 AA.
AC Q92R25;
DT 01-DEC-2001 (TREMUREL.19, Created)
DT 01-DEC-2001 (TREMUREL.19, Last sequence update)
DT 01-MAR-2002 (TREMUREL.20, Last annotation update)
DE Chemotaxis protein (Motility protein D).
GN MOTD OR R00676 OR SMC03044.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1021;
RX MEDLINE=21396507; PubMed-11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boisdard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaire V., Masuy D.,
RA Pohl T., Portetle D., Puenhler A., Purnelle B., Ranspiger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.,
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL: AL591784; CAC45248.1; -.
KW Complete proteome.
SQ SEQUENCE 475 AA; 49124 MW; 8177547429DD4425 CRC64;

Query Match 49.1%; Score 52; DB 16; Length 475;
Best Local Similarity 52.9%; Pred. No. 5.9;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 DGSGEQPRGGGPTSSQI 18
| | | | | | | | | |
DB 435 DGCGRPRDGGRAATER 451

RESULT 10

Q9N8R6 PRELIMINARY; PRT; 658 AA.
AC Q9N8R6;
DT 01-OCT-2000 (TREMUREL.15, Created)
DT 01-OCT-2000 (TREMUREL.15, Last sequence update)
DT 01-JUN-2002 (TREMUREL.21, Last annotation update)
DE Possible putative cell division related protein.
GN CHRI.177.
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=TREU927;
RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,
RA Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,
RA Gerrard C., Rajandream M.A., Barrett B.G.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
CC EMBL: AL359782; CAB95467.1; -.
DR HSSP: P25685; IHDJ.
DR InterPro: IPR001623; DnaJ_N.
DR InterPro: IPR003095; Hsp_DnaJ.
DR InterPro: IPR001005; Myb_DnaJ_binding.

DR Pfam: PF00226; DnaJ_1.
DR Pfam: PF00249; myb_DnaJ-binding_1.
DR PRINTS: PR00625; DNAJPROTEIN.
DR SMART: SM00271; DnaJ_1.
DR SMART: SM00395; SANT_1.
DR PROSITE: PS50076; DnaJ_2; 1.
KW Cell division; Nuclear protein.
SQ SEQUENCE 658 AA; 75711 MW; C374319479C8ADEFCRC64;

Query Match 48.1%; Score 51; DB 5; Length 658;
Best Local Similarity 58.8%; Pred. No. 12;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 DGSGEQPRGGGPTSSQI 18
| | | | | | | | | |
DB 88 DGSGEQPRGGGPTSSQI 104

RESULT 11

Q9SBR7 PRELIMINARY; PRT; 213 AA.
AC Q9SBR7;
DT 01-MAY-2000 (TREMUREL.13, Created)
DT 01-MAY-2000 (TREMUREL.13, Last sequence update)
DT 01-DEC-2001 (TREMUREL.19, Last annotation update)
DE EndoGRP5 protein.
GN ENODGRP5.
OS Medicago varia.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX NCBI_TaxID=36902;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=ROOT NODULES;
RX MEDLINE=20120383; PubMed-10656590;
RA Jimenez-Zurdo J.I., Fuglier F., Crespi M.D., Kondorosi A.;
RT "Expression profiles of 22 novel molecular markers for organogenetic
RT pathways acting in alfalfa nodule development."
RL Mol. Plant Microbe Interact. 13:96-106(2000).
DR EMBL: AJ248329; CAB65282.1; -.
KW SEQUENCE 213 AA; 23149 MW; 137C629EDD19872A CRC64;

Query Match 47.2%; Score 50; DB 10; Length 213;
Best Local Similarity 52.9%; Pred. No. 5;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 GSGEQPRGGGPTSSQI 19
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DB 90 GSGEQPRGGGPTSSQI 106

RESULT 12

Q918P0 PRELIMINARY; PRT; 495 AA.
AC Q918P0;
DT 01-DEC-2001 (TREMUREL.19, Created)
DT 01-DEC-2001 (TREMUREL.19, Last sequence update)
DT 01-DEC-2001 (TREMUREL.19, Last annotation update)
DE Latency associated antigen.
GN ORF73.
OS Ovine herpesvirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae.
OX NCBI_TaxID=10398;
RN [1]
RP SEQUENCE FROM N.A.
RA Coulter L.J., Reid H.W.;
RT "Isolation and expression of three open reading frames (ORFs) from
RT ovine herpesvirus 2."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF410647; AAU05844.1; -.
SQ SEQUENCE 495 AA; 49366 MW; 2D3B70651085693FCRC64;

Query Match 47.2%; Score 50; DB 12; Length 495;
 Best Local Similarity 56.2%; Pred. No. 13;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 3 GSGEOPRGCGPRTSSQ 18
 DB 255 GEGEGRGCGGPGGEE 270

RESULT 13

O9M221 PRELIMINARY; PRT; 743 AA.
 AC O9M221;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE Hypothetical 82.6 kDa protein.
 GN T8B10.40.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eustoidia II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,
 RA Lemke K., Mayer K.F.X., Queller F., Salioubat M.;
 RL Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL138646; CAB81824.1; -;
 DR InterPro: IPR000977; DNA_ligase.
 DR PROSITE: PS00697; DNA_LIGASE_A1; UNKNOWN_1.
 KM Hypothetical protein.
 SQ SEQUENCE 743 AA; 82639 MW; EB30CA4906AC06E2 CRC64;

Query Match 47.2%; Score 50; DB 10; Length 743;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 SGEOPRGCG 12
 DB 725 SGEOPRGCG 733

RESULT 14

O96AV4 PRELIMINARY; PRT; 473 AA.
 AC O96AV4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical 50.8 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LYMPH;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC016681; AAH16681.1; -;
 DR InterPro: IPR000449; UBA_domain.
 KM Hypothetical protein.
 SQ SEQUENCE 473 AA; 50750 MW; D27DAD437DA98AA9 CRC64;

Query Match 46.7%; Score 49.5; DB 4; Length 473;
 Best Local Similarity 52.6%; Pred. No. 15;
 Matches 10; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

OY 3 GSGEOPRGCG-PRSSQIM 20
 DB 155 GAGDEARGGSPSTQTTL 173

RESULT 15

O96JL4 PRELIMINARY; PRT; 715 AA.
 AC O96JL4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE KIAA1811 protein (Fragment).
 GN KIAA1811.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=21245130; PubMed=11347906;
 RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XX.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro."
 RL DNA Res. 8:85-95(2001).
 RL EMBL; AB058714; BAB47440.1; -;
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR000449; UBA_domain.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 715 AA; 78499 MW; B90F6EE113C418A5 CRC64;

Query Match 46.7%; Score 49.5; DB 4; Length 715;
 Best Local Similarity 52.6%; Pred. No. 23;
 Matches 10; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

OY 3 GSGEOPRGCG-PRSSQIM 20
 DB 397 GAGDEARGGSPSTQTTL 415

Search completed: January 7, 2003, 12:30:49
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:29:33 : Search time 140 seconds
(without alignments)
92.105 Million cell updates/sec

Title: US-09-876-204-3

Perfect score: 106
Sequence: 1 MDGSGEOPRGCGPTSSSEQIM 20

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents-AA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	20	22	US-09-876-204-3
2	106	100.0	70	1	PCT-US99-24747-1
3	106	100.0	70	1	PCT-US99-24747-5
4	106	100.0	70	15	US-09-177-315-1
5	106	100.0	70	15	US-09-177-315-5
6	106	100.0	78	1	PCT-US99-24747-3

7	106	100.0	78	1	PCT-US99-24747-7	Sequence 7, Appli
8	106	100.0	78	15	US-09-177-315-3	Sequence 3, Appli
9	106	100.0	78	15	US-09-177-315-7	Sequence 7, Appli
10	106	100.0	131	1	PCT-US99-05359-2	Sequence 2, Appli
11	106	100.0	131	16	US-09-266-465-2	Sequence 2, Appli
12	106	100.0	135	1	PCT-US02-06951-242	Sequence 242, App
13	106	100.0	135	24	US-10-092-750-242	Sequence 242, App
14	106	100.0	143	21	US-09-791-537-52874	Sequence 52874, A
15	106	100.0	143	27	US-60-350-061-261	Sequence 261, App
16	106	100.0	164	21	US-09-791-537-105329	Sequence 105329,
17	106	100.0	192	1	PCT-US98-19765-46	Sequence 46, Appl
18	106	100.0	192	1	PCT-US99-05359-4	Sequence 4, Appli
19	106	100.0	192	1	PCT-US99-24747-112	Sequence 12, Appl
20	106	100.0	192	5	US-08-112-208B-6	Sequence 6, Appli
21	106	100.0	192	5	US-08-160-067-7	Sequence 7, Appli
22	106	100.0	192	6	US-08-248-819-6	Sequence 6, Appli
23	106	100.0	192	7	US-08-320-157-13	Sequence 13, Appl
24	106	100.0	192	8	US-08-470-865-13	Sequence 8, Appli
25	106	100.0	192	8	US-08-483-233-2	Sequence 2, Appli
26	106	100.0	192	8	US-08-483-233-9	Sequence 9, Appli
27	106	100.0	192	8	US-08-483-233A-2	Sequence 2, Appli
28	106	100.0	192	8	US-08-483-233A-9	Sequence 9, Appli
29	106	100.0	192	8	US-08-485-934-2	Sequence 2, Appli
30	106	100.0	192	8	US-08-485-934-9	Sequence 9, Appli
31	106	100.0	192	9	US-08-508-550-2	Sequence 2, Appli
32	106	100.0	192	13	US-08-946-039-46	Sequence 46, Appl
33	106	100.0	192	15	US-09-177-315-12	Sequence 12, Appl
34	106	100.0	192	16	US-09-266-465-4	Sequence 4, Appli
35	106	100.0	192	17	US-09-379-820-2	Sequence 2, Appli
36	106	100.0	192	17	US-09-379-820-9	Sequence 9, Appli
37	106	100.0	192	17	US-09-379-820A-2	Sequence 2, Appli
38	106	100.0	192	17	US-09-379-820A-9	Sequence 9, Appli
39	106	100.0	192	18	US-09-456-357-26	Sequence 26, Appl
40	106	100.0	192	19	US-09-587-473-19	Sequence 19, Appl
41	106	100.0	192	20	US-09-617-878-8	Sequence 8, Appli
42	106	100.0	192	20	US-09-693-200-13	Sequence 13, Appl
43	106	100.0	192	20	US-09-693-714-7	Sequence 7, Appli
44	106	100.0	192	21	US-09-791-537-3979	Sequence 3979, Ap
45	106	100.0	192	21	US-09-791-537-127903	Sequence 127903,

ALIGNMENTS

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RESULT 1
US-09-876-204-3
: Sequence 3, Application US/09876204
: GENERAL INFORMATION:
: APPLICANT: Gordon C. Shore et al.
: TITLE OF INVENTION: BAX-MEDIATED APOPTOSIS MODULATING
: FILE OF INVENTION: REAGENTS AND METHODS
: TITLE REFERENCE: 50013/011001
: CURRENT APPLICATION NUMBER: US/09/876, 204
: PRIOR FILING DATE: 2001-06-06
: PRIOR APPLICATION NUMBER: 09/166, 028
: PRIOR FILING DATE: 1998-10-05
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 20
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-876-204-3
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QY	1	MDGSGEOPRGCGPTSSSEQIM 20
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RESULT 2
PCT-US99-24747-1
; Sequence 1, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-24747-1

Query Match 100.0%; Score 106; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGGPTSSSEQIM 20
Db 1 MDGSGEOPRGGPTSSSEQIM 20

RESULT 3
PCT-US99-24747-5
; Sequence 5, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 70
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; ORGANISM: Homo sapiens
PCT-US99-24747-5

Query Match 100.0%; Score 106; DB 1; Length 70;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGGPTSSSEQIM 20
Db 1 MDGSGEOPRGGPTSSSEQIM 20

RESULT 4
US-09-177-315-1
; Sequence 1, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-5756
; CURRENT APPLICATION NUMBER: US/09/177,315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-177-315-1

Query Match 100.0%; Score 106; DB 15; Length 70;

Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-177-315-5
; Sequence 5, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-5756
; CURRENT APPLICATION NUMBER: US/09/177,315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
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; ORGANISM: Homo sapiens
US-09-177-315-5

Query Match 100.0%; Score 106; DB 15; Length 70;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDGSGEOPRGGPTSSSEQIM 20
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; Sequence 3, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-24747-3

Query Match 100.0%; Score 106; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MDGSGEOPRGGPTSSSEQIM 20

RESULT 7
PCT-US99-24747-7
; Sequence 7, Application PC/TUS9924747
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; APPLICANT: Easton, Rachael M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-1754
; CURRENT APPLICATION NUMBER: PCT/US99/24747
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 34

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-24747-7
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Query Match
Best Local Similarity 100.0%; Score 106; DB 1; Length 78;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 1 MDGSGEQPRGGGPTSSSEQIM 20
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Db 1 MDGSGEQPRGGGPTSSSEQIM 20
```

```
RESULT 8
US-09-177-315-3
; Sequence 3, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-5756
; CURRENT APPLICATION NUMBER: US/09/177,315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-177-315-3
```

```
Query Match
Best Local Similarity 100.0%; Score 106; DB 15; Length 78;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 MDGSGEQPRGGGPTSSSEQIM 20
|
Db 1 MDGSGEQPRGGGPTSSSEQIM 20
```

```
RESULT 9
US-09-177-315-7
; Sequence 7, Application US/09177315
; GENERAL INFORMATION:
; APPLICANT: Johnson Jr., Eugene M.
; TITLE OF INVENTION: Neuroprotective Truncated BAX Polypeptides
; FILE REFERENCE: 6029-5756
; CURRENT APPLICATION NUMBER: US/09/177,315
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-177-315-7
```

```
Query Match
Best Local Similarity 100.0%; Score 106; DB 15; Length 78;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 1 MDGSGEQPRGGGPTSSSEQIM 20
|
Db 1 MDGSGEQPRGGGPTSSSEQIM 20
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```
RESULT 10
PCT-US99-05359-2
; Sequence 2, Application PC/TUS9905359
```

```
; GENERAL INFORMATION:
; APPLICANT: MCDONNELL, TIMOTHY J.
; APPLICANT: SWISHER, STEVEN G.
; APPLICANT: FANG, BINGLIANG
; APPLICANT: BROCKHEIMER, ELIZABETH
; APPLICANT: SAKKISS, MONA
; APPLICANT: JI, LIN
; APPLICANT: ROTH, JACK A.
; TITLE OF INVENTION: INDUCTION OF APOPTIC OR CYTOTOXIC GENE EXPRESSION BY
; FILE REFERENCE: INGN:088/INGN:088P
; CURRENT APPLICATION NUMBER: PCT/US99/05359
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: 60/077,541
; EARLIER FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Human
PCT-US99-05359-2
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```
Query Match
Best Local Similarity 100.0%; Score 106; DB 1; Length 131;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 MDGSGEQPRGGGPTSSSEQIM 20
|
Db 1 MDGSGEQPRGGGPTSSSEQIM 20
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RESULT 11
US-09-266-465-2
; Sequence 2, Application US/09266465
; GENERAL INFORMATION:
; APPLICANT: MCDONNELL, TIMOTHY J.
; APPLICANT: SWISHER, STEVEN G.
; APPLICANT: FANG, BINGLIANG
; APPLICANT: BROCKHEIMER, ELIZABETH
; APPLICANT: SAKKISS, MONA
; APPLICANT: JI, LIN
; APPLICANT: ROTH, JACK A.
; TITLE OF INVENTION: INDUCTION OF APOPTIC OR CYTOTOXIC GENE EXPRESSION BY
; FILE REFERENCE: INGN:088/INGN:088P
; CURRENT APPLICATION NUMBER: US/09/266,465
; CURRENT FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: 60/077,541
; EARLIER FILING DATE: 1998-03-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Human
US-09-266-465-2
```

```
Query Match
Best Local Similarity 100.0%; Score 106; DB 16; Length 131;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 1 MDGSGEQPRGGGPTSSSEQIM 20
|
Db 1 MDGSGEQPRGGGPTSSSEQIM 20
```

```
RESULT 12
PCT-US02-06951-242
; Sequence 242, Application PC/TUS0206951
; GENERAL INFORMATION:
; APPLICANT: Phyllos, Inc.
; TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
```

FILE REFERENCE: 50036/050M02
CURRENT APPLICATION NUMBER: PCT/US02/06951
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US 60/274,526
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 242
LENGTH: 135
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-06951-242

Query Match 100.0%; Score 106; DB 1; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSSEQIM 20
Db 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 13
US-10-092-750-242
Sequence 242, Application US/10092750
GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Alpin, Julia
APPLICANT: Wright, Martin C.
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
FILE REFERENCE: 50036/050002
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: US 60/274,526
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 242
LENGTH: 135
TYPE: PRT
ORGANISM: Homo sapiens
US-10-092-750-242

Query Match 100.0%; Score 106; DB 24; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSSEQIM 20
Db 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 14
US-09-791-537-52874
Sequence 52874, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 52874
LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-537-52874

Query Match 100.0%; Score 106; DB 21; Length 143;

Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSSEQIM 20
Db 1 MDGSGEQPRGGGPTSSSEQIM 20

RESULT 15
US-60-350-061-261
Sequence 261, Application US/60350061
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT INTERACT WITH SRC TYROSINE KINASES AND THE SRC TYROSINE KINASES
FILE REFERENCE: D0185
CURRENT APPLICATION NUMBER: US/60/350,061
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 981
SOFTWARE: PatentIn version 3.0
SEQ ID NO 261
LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
US-60-350-061-261

Query Match 100.0%; Score 106; DB 27; Length 143;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSGEQPRGGGPTSSSEQIM 20
Db 1 MDGSGEQPRGGGPTSSSEQIM 20

Search completed: January 7, 2003, 12:36:30
Job time : 141 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 12:29:58 ; Search time 11.7949 Seconds
(without alignments)
120.181 Million cell updates/sec

Title: US-09-876-204-3

Perfect score: 106
Sequence: 1 MDGSGEPRGCGPTSSSEQIM 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262191 seqs, 70875818 residues

Total number of hits satisfying chosen parameters: 262191

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*

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6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	100.0	192	1	PCT-US02-38191-5
2	106	100.0	192	6	US-10-306-878-5
3	101	95.3	191	6	US-10-196-793A-46
4	52	49.1	402	1	PCT-US02-06001-32
5	52	49.1	402	6	US-10-274-177-18
6	52	49.1	402	6	US-10-087-080-32
7	47	44.3	73	1	PCT-US02-32727-25717
8	47	44.3	73	1	PCT-US02-32727-29374
9	47	44.3	73	6	US-10-057-498-25717
10	47	44.3	220	5	US-09-724-676A-55403
11	47	44.3	220	5	US-09-724-676A-55403
12	45	42.5	94	1	PCT-US02-32727-10714
13	45	42.5	94	6	US-10-057-498-10714
14	44	41.5	131	6	US-10-276-774-1847
15	44	41.5	256	5	US-09-724-676-64338
16	44	41.5	256	5	US-09-724-676-64341
17	44	41.5	256	5	US-09-724-676-64345
18	44	41.5	256	5	US-09-724-676-64346
19	44	41.5	256	5	US-09-724-676A-64338
20	44	41.5	256	5	US-09-724-676A-64341
21	44	41.5	256	5	US-09-724-676A-64345
22	44	41.5	256	5	US-09-724-676A-64346
23	43	40.6	352	5	US-09-724-676-50097
24	43	40.6	352	5	US-09-724-676-50098
25	43	40.6	352	5	US-09-724-676A-50097
26	43	40.6	352	5	US-09-724-676A-50098

27	43	40.6	357	5	US-09-724-676-50091	Sequence 50091, A
28	43	40.6	357	5	US-09-724-676-50092	Sequence 50092, A
29	43	40.6	357	5	US-09-724-676A-50091	Sequence 50091, A
30	43	40.6	357	5	US-09-724-676A-50092	Sequence 50092, A
31	43	40.6	402	5	US-09-724-676-50099	Sequence 50099, A
32	43	40.6	402	5	US-09-724-676-50100	Sequence 50100, A
33	43	40.6	402	5	US-09-724-676A-50099	Sequence 50099, A
34	43	40.6	402	5	US-09-724-676A-50100	Sequence 50100, A
35	43	40.6	407	5	US-09-724-676-50093	Sequence 50093, A
36	43	40.6	407	5	US-09-724-676-50094	Sequence 50094, A
37	43	40.6	407	5	US-09-724-676A-50093	Sequence 50093, A
38	43	40.6	407	5	US-09-724-676A-50094	Sequence 50094, A
39	43	40.6	419	6	US-10-302-267-126	Sequence 126, App
40	43	40.6	477	5	US-09-724-676A-91247	Sequence 91247, A
41	43	40.6	477	5	US-09-724-676A-91247	Sequence 91247, A
42	43	40.6	486	5	US-09-724-676-50096	Sequence 50096, A
43	43	40.6	486	5	US-09-724-676A-50096	Sequence 50096, A
44	43	40.6	491	5	US-09-724-676-50101	Sequence 50101, A
45	43	40.6	491	5	US-09-724-676-50102	Sequence 50102, A

ALIGNMENTS

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RESULT 1
PCT-US02-38191-5
; Sequence 5, Application PC/TUS0238191
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Reed, John C.
; APPLICANT: Guo, Bin
; TITLE OF INVENTION: Methods for Identifying Modulators of
; FILE REFERENCE: FP-LJ 5483
; CURRENT APPLICATION NUMBER: PCT/US02/38191
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US 60/334,149
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-38191-5

Query Match          100.0%; Score 106; DB 1; Length 192;
Best local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MDGSGEPRGCGPTSSSEQIM 20
        |||
Db       1 MDGSGEPRGCGPTSSSEQIM 20

RESULT 2
US-10-306-878-5
; Sequence 5, Application US/10306878
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Guo, Bin
; TITLE OF INVENTION: Methods for Identifying Modulators of
; FILE REFERENCE: P-LJ 5355
; CURRENT APPLICATION NUMBER: US/10/306,878
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US 60/334,149
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 192
; TYPE: PRT
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```
OY      3 GSGEOPRGCGPTSSSEQ 19
      1 111 1111 : 1 1
Db      61 GDGEQSGAGGPGCAAEAI 77

RESULT 7
PCT-US02-32727-25717
; Sequence 25717, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yann
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; APPLICANT: Barth, Brenda
; FILE REFERENCE: 210121.514c1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 125717
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Propionl acnes
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (44)
; OTHER INFORMATION: Xaa = Any Amino Acid
PCT-US02-32727-25717

Query Match      44.3%: Score 47; DB 1; Length 73;
Best Local Similarity 44.4%: Pred. No. 16;
Matches      8; Conservative      2; Mismatches      8; Indels      0; Gaps      0;

OY      1 MDGSGEOPRGCGPTSSSEQ 18
      1 111 1111 : 1 1
Db      45 LDGDGHRPAGGDEBRRQ 62

RESULT 8
PCT-US02-32727-29374
; Sequence 29374, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yann
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; APPLICANT: Barth, Brenda
; FILE REFERENCE: 210121.514c1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 29374
; LENGTH: 73
; TYPE: PRT
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```
; ORGANISM: Propionibacterium acnes
PCT-US02-32727-29374

Query Match      44.3%: Score 47; DB 1; Length 73;
Best Local Similarity 44.4%: Pred. No. 16;
Matches      8; Conservative      2; Mismatches      8; Indels      0; Gaps      0;

OY      1 MDGSGEOPRGCGPTSSSEQ 18
      1 111 1111 : 1 1
Db      45 LDGDGHRPAGGDEBRRQ 62

RESULT 9
US-10-057-498-25717
; Sequence 25717, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Persing, David
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 25717
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Propionl acnes
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (44)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-057-498-25717

Query Match      44.3%: Score 47; DB 6; Length 73;
Best Local Similarity 44.4%: Pred. No. 16;
Matches      8; Conservative      2; Mismatches      8; Indels      0; Gaps      0;
```

```
OY      1 MDGSGEOPRGCGPTSSSEQ 18
      1 111 1111 : 1 1
Db      45 LDGDGHRPAGGDEBRRQ 62

RESULT 10
US-09-724-676-55403
; Sequence 55403, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55403
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-55403

Query Match      44.3%: Score 47; DB 5; Length 220;
Best Local Similarity 72.7%: Pred. No. 42;
Matches      8; Conservative      0; Mismatches      3; Indels      0; Gaps      0;

OY      3 GSGEOPRGCGP 13
      1 1 111111
Db      76 GRCASPRGCGP 86

RESULT 11
US-09-724-676A-55403
; Sequence 55403, Application US/09724676A
; GENERAL INFORMATION:
```

```
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55403
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-55403
```

```
Query Match 44.3%; Score 47; DB 5; Length 220;
Best Local Similarity 72.7%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 3 GSGEQPRGGCP 13
| | | | | | | |
DB 76 GRCASPRGGCP 86
```

```
RESULT 12
PCT-US02-32727-10714
; Sequence 10714, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhalla, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yann
; APPLICANT: Wang, Shiyang
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Derrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514CI
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 10714
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-10714
```

```
Query Match 42.5%; Score 45; DB 1; Length 94;
Best Local Similarity 61.5%; Pred. No. 37;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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```
QY 8 PRGGPTSSQIM 20
| | | | | | | |
DB 26 PRAGGPTSSPELV 38
```

```
RESULT 13
US-10-057-498-10714
; Sequence 10714, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 10714
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; LENGTH: 94
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-10714
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```
Query Match 42.5%; Score 45; DB 6; Length 94;
Best Local Similarity 61.5%; Pred. No. 37;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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```
QY 8 PRGGPTSSQIM 20
| | | | | | | |
DB 26 PRAGGPTSSPELV 38
```

```
RESULT 14
US-10-276-774-1847
; Sequence 1847, Application US/10276774
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1847
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-1847
```

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Query Match 41.5%; Score 44; DB 6; Length 131;
Best Local Similarity 45.5%; Pred. No. 68;
Matches 10; Conservative 3; Mismatches 3; Indels 6; Gaps 1;
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QY 2 DGSGEQ-----PRGGPTSE 17
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DB 64 EGAGSPPPGCPRGSSSSE 85
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RESULT 15
US-09-724-676-64338
; Sequence 64338, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64338
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-64338
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Query Match 41.5%; Score 44; DB 5; Length 256;
Best Local Similarity 50.0%; Pred. No. 1,2e+02;
Matches 10; Conservative 3; Mismatches 5; Indels 2; Gaps 1;
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QY 1 MDGSGEQPRGC--GPTSSQ 18
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DB 139 MDGDPREPREFWPTSSDE 158
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Search completed: January 7, 2003, 12:36:59
Job time : 11.7949 secs
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